



OIE

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Input Set : A:\Seq_List_for_P2830P1C8.wpd
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Does Not Comply
Corrected Diskette Needed

3 <110> APPLICANT: Baker, Kevin P.
4 Botstein, David
5 Desnoyers, Luc
6 Eaton, Dan L.
7 Ferrara, Napoleone
8 Fong, Sherman
9 Gao, Wei-Qiang
10 Goddard, Audrey
11 Godowski, Paul J.
12 Grimaldi, Christopher J.
13 Gurney, Austin L.
14 Hillan, Kenneth J.
15 Pan, James
16 Paoni, Nicholas F.
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Review the Sequence Listing to insure a corresponding
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::2795 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:45
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::2818 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:47
::2821 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:47
::2831 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:48
::2834 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:48
::3957 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:59

VERIFICATION SUMMARY
PATENT APPLICATION: US/10/006,041

DATE: 01/24/2002
TIME: 14:23:29

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U:4122 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:63
U:4158 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:63
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U:4188 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:64
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U:4201 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:65
U:4211 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:66
U:4214 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:66
U:4694 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:73
U:4697 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:73
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U:4723 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:75
U:5092 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:80
U:5095 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:80
U:5108 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:81
U:5118 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:82
U:5121 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:82
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U:6146 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:96
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U:6159 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:97
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U:6887 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:105
U:6897 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:106
U:6900 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:106
U:6910 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:107
U:6913 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:107
U:6923 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:108
U:6926 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:108

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/006,041

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::7092 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:114
::7095 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:114
::7473 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:119
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::20939 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:377
::22554 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:422

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Thr	Phe	Gly	Cys	Phe	Ala	Thr	Cys	Arg	Ala	Ser	Ala	Trp	Met	Leu
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Lys	Leu	Tyr	Ala	Met	Phe	Leu	Thr	Leu	Val	Phe	Leu	Val	Glu	Leu
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Val	Ala	Ala	Ile	Val	Gly	Phe	Val	Phe	Arg	His	Glu	Ile	Lys	Asn
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Ser	Phe	Lys	Asn	Asn	Tyr	Glu	Lys	Ala	Leu	Lys	Gln	Tyr	Asn	Ser
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Thr	Gly	Asp	Tyr	Arg	Ser	His	Ala	Val	Asp	Lys	Ile	Gln	Asn	Thr
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Glu	Asp	Cys	Thr	Pro	Gln	Arg	Asp	Ala	Asp	Lys	Val	Asn	Asn	Glu
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Gly	Cys	Phe	Ile	Lys	Val	Met	Thr	Ile	Ile	Glu	Ser	Glu	Met	Gly
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<222> 22-26, 50-54, 113-117
<223> Casein Kinase II Phosphorylation Site.

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35 40 45
Cys Arg Asp Asp Ser Gly Thr Asp Asp Ser Val Asp Thr Gln Gln
50 55 60
Gln Gln Ala Glu Asn Ser Ala Val Pro Thr Ala Asp Thr Arg Ser
65 70 75
Gln Pro Arg Asp Pro Val Arg Pro Pro Arg Arg Gly Arg Gly Pro
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<223> Prokaryotic Membrane Lipoprotein Lipid Attachment Site.

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<223> Casein Kinase II Phosphorylation Site.

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35 40 45
Ala Arg Thr Phe Asp Lys Lys Gly Phe His Val Ile Ala Ala Cys
50 55 60
Leu Thr Glu Ser Gly Ser Thr Ala Leu Lys Ala Glu Thr Ser Glu
65 70 75
Arg Leu Arg Thr Val Leu Leu Asp Val Thr Asp Pro Glu Asn Val
80 85 90
Lys Arg Thr Ala Gln Trp Val Lys Asn Gln Val Gly Glu Lys Gly
95 100 105
Leu Trp Gly Leu Ile Asn Asn Ala Gly Val Pro Gly Val Leu Ala
110 115 120
Pro Thr Asp Trp Leu Thr Leu Glu Asp Tyr Arg Glu Pro Ile Glu
125 130 135
Val Asn Leu Phe Gly Leu Ile Ser Val Thr Leu Asn Met Leu Pro
140 145 150
Leu Val Lys Lys Ala Gln Gly Arg Val Ile Asn Val Ser Ser Val
155 160 165
Gly Gly Arg Leu Ala Ile Val Gly Gly Tyr Thr Pro Ser Lys
170 175 180
Tyr Ala Val Glu Gly Phe Asn Asp Ser Leu Arg Arg Asp Met Lys
185 190 195

Ala Phe Gly Val His Val Ser Cys Ile Glu Pro Gly Leu Phe Lys
 200 205 210
 Thr Asn Leu Ala Asp Pro Val Lys Val Ile Glu Lys Lys Leu Ala
 215 220 225
 Ile Trp Glu Gln Leu Ser Pro Asp Ile Lys Gln Gln Tyr Gly Glu
 230 235 240
 Gly Tyr Ile Glu Lys Ser Leu Asp Lys Leu Lys Gly Asn Lys Ser
 245 250 255
 Tyr Val Asn Met Asp Leu Ser Pro Val Val Glu Cys Met Asp His
 260 265 270
 Ala Leu Thr Ser Leu Phe Pro Lys Thr His Tyr Ala Ala Gly Lys
 275 280 285
 Asp Ala Lys Ile Phe Trp Ile Pro Leu Ser His Met Pro Ala Ala
 290 295 300
 Leu Gln Asp Phe Leu Leu Lys Gln Lys Ala Glu Leu Ala Asn
 305 310 315
 Pro Lys Ala Val

<210> 11
 <211> 2720
 <212> DNA
 <213> Homo sapines

<400> 11
 gcgggctgtt gacggcgctg cgatggctgc ctgcgagggc aggagaagcg 50
 gagctctcggtt ttcctctcag tcggacttcc tgacgcccgc agtggggcggg 100
 gccccttggg ccgtcgccac cactgtagtc atgtacccac cgccgcccgc 150
 gccgcctcat cgggacttca tctcggtgac gctgagctt ggcgagagact 200
 atgacaacag caagagttgg cggcggcgct cgtgctggag gaaatggaag 250
 caactgtcga gattgcagcg gaatatgatt ctcttcctcc ttgcctttct 300
 gctttctgt ggactcctct tctacatcaa cttggctgac cattggaaag 350
 ctctggcttt caggctagag gaagagcaga agatgaggcc agaaattgct 400
 gggtaaaac cagcaaatcc acccgcttta ccagctcctc agaaggcgga 450
 caccgaccct gagaacttac ctgagatttc gtcacagaag acacaaagac 500
 acatccagcg gggaccaccc cacctgcaga ttagacccccc aagccaagac 550
 ctgaaggatg ggacccagga ggaggccaca aaaaggcaag aagccccctgt 600
 ggatccccgc ccggaaggag atccgcagag gacagtcatac agctggaggg 650

gagcgggtgat cgagcctgag cagggcacccg agctcccttc aagaagagca 700
gaagtgccca ccaagcctcc cctgccacccg gccaggacac agggcacacc 750
agtgcatctg aactatcgcc agaagggcgt gattgacgac ttccctgcatt 800
catggaaagg ataccgcaag tttgcattggg gccatgacga gctgaagcct 850
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cctcctggcc gccccgcagg gggcttgag ggctggacgg caagtccgtc 2650
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ttgatttgct ctaaccgcaa 2720

<210> 12
<211> 699
<212> PRT
<213> Homo sapiens

<220>
<221> TRANSMEM
<222> 21-40 and 84-105
<223> Transmembrane Domain (type II)

<400> 12
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Gln Ser Asp Phe Leu Thr Pro Pro Val Gly Gly Ala Pro Trp Ala
20 25 30
Val Ala Thr Thr Val Val Met Tyr Pro Pro Pro Pro Pro Pro Pro
35 40 45
His Arg Asp Phe Ile Ser Val Thr Leu Ser Phe Gly Glu Ser Tyr
50 55 60
Asp Asn Ser Lys Ser Trp Arg Arg Ser Cys Trp Arg Lys Trp
65 70 75
Lys Gln Leu Ser Arg Leu Gln Arg Asn Met Ile Leu Phe Leu Leu
80 85 90
Ala Phe Leu Leu Phe Cys Gly Leu Leu Phe Tyr Ile Asn Leu Ala
95 100 105

Asp His Trp Lys Ala Leu Ala Phe Arg Leu Glu Glu Glu Gln Lys
 110 115 120
 Met Arg Pro Glu Ile Ala Gly Leu Lys Pro Ala Asn Pro Pro Val
 125 130 135
 Leu Pro Ala Pro Gln Lys Ala Asp Thr Asp Pro Glu Asn Leu Pro
 140 145 150
 Glu Ile Ser Ser Gln Lys Thr Gln Arg His Ile Gln Arg Gly Pro
 155 160 165
 Pro His Leu Gln Ile Arg Pro Pro Ser Gln Asp Leu Lys Asp Gly
 170 175 180
 Thr Gln Glu Glu Ala Thr Lys Arg Gln Glu Ala Pro Val Asp Pro
 185 190 195
 Arg Pro Glu Gly Asp Pro Gln Arg Thr Val Ile Ser Trp Arg Gly
 200 205 210
 Ala Val Ile Glu Pro Glu Gln Gly Thr Glu Leu Pro Ser Arg Arg
 215 220 225
 Ala Glu Val Pro Thr Lys Pro Pro Leu Pro Pro Ala Arg Thr Gln
 230 235 240
 Gly Thr Pro Val His Leu Asn Tyr Arg Gln Lys Gly Val Ile Asp
 245 250 255
 Val Phe Leu His Ala Trp Lys Gly Tyr Arg Lys Phe Ala Trp Gly
 260 265 270
 His Asp Glu Leu Lys Pro Val Ser Arg Ser Phe Ser Glu Trp Phe
 275 280 285
 Gly Leu Gly Leu Thr Leu Ile Asp Ala Leu Asp Thr Met Trp Ile
 290 295 300
 Leu Gly Leu Arg Lys Glu Phe Glu Glu Ala Arg Lys Trp Val Ser
 305 310 " 315
 Lys Lys Leu His Phe Glu Lys Asp Val Asp Val Asn Leu Phe Glu
 320 325 330
 Ser Thr Ile Arg Ile Leu Gly Gly Leu Leu Ser Ala Tyr His Leu
 335 340 345
 Ser Gly Asp Ser Leu Phe Leu Arg Lys Ala Glu Asp Phe Gly Asn
 350 355 360
 Arg Leu Met Pro Ala Phe Arg Thr Pro Ser Lys Ile Pro Tyr Ser
 365 370 375
 Asp Val Asn Ile Gly Thr Gly Val Ala His Pro Pro Arg Trp Thr
 380 385 390
 Ser Asp Ser Thr Val Ala Glu Val Thr Ser Ile Gln Leu Glu Phe

395	400	405
Arg Glu Leu Ser Arg Leu Thr Gly Asp Lys Lys Phe Gln Glu Ala		
410	415	420
Val Glu Lys Val Thr Gln His Ile His Gly Leu Ser Gly Lys Lys		
425	430	435
Asp Gly Leu Val Pro Met Phe Ile Asn Thr His Ser Gly Leu Phe		
440	445	450
Thr His Leu Gly Val Phe Thr Leu Gly Ala Arg Ala Asp Ser Tyr		
455	460	465
Tyr Glu Tyr Leu Leu Lys Gln Trp Ile Gln Gly Gly Lys Gln Glu		
470	475	480
Thr Gln Leu Leu Glu Asp Tyr Val Glu Ala Ile Glu Gly Val Arg		
485	490	495
Thr His Leu Leu Arg His Ser Glu Pro Ser Lys Leu Thr Phe Val		
500	505	510
Gly Glu Leu Ala His Gly Arg Phe Ser Ala Lys Met Asp His Leu		
515	520	525
Val Cys Phe Leu Pro Gly Thr Leu Ala Leu Gly Val Tyr His Gly		
530	535	540
Leu Pro Ala Ser His Met Glu Leu Ala Gln Glu Leu Met Glu Thr		
545	550	555
Cys Tyr Gln Met Asn Arg Gln Met Glu Thr Gly Leu Ser Pro Glu		
560	565	570
Ile Val His Phe Asn Leu Tyr Pro Gln Pro Gly Arg Arg Asp Val		
575	580	585
Glu Val Lys Pro Ala Asp Arg His Asn Leu Leu Arg Pro Glu Thr		
590	595	600
Val Glu Ser Leu Phe Tyr Leu Tyr Arg Val Thr Gly Asp Arg Lys		
605	610	615
Tyr Gln Asp Trp Gly Trp Glu Ile Leu Gln Ser Phe Ser Arg Phe		
620	625	630
Thr Arg Val Pro Ser Gly Gly Tyr Ser Ser Ile Asn Asn Val Gln		
635	640	645
Asp Pro Gln Lys Pro Glu Pro Arg Asp Lys Met Glu Ser Phe Phe		
650	655	660
Leu Gly Glu Thr Leu Lys Tyr Leu Phe Leu Leu Phe Ser Asp Asp		
665	670	675
Pro Asn Leu Leu Ser Leu Asp Ala Tyr Val Phe Asn Thr Glu Ala		
680	685	690

His Pro Leu Pro Ile Trp Thr Pro Ala
695

<210> 13
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 13
cgccagaagg gcgtgattga cgtc 24

<210> 14
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 14
ccatccttct tcccagacag gccg 24

<210> 15
<211> 44
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-44
<223> Synthetic construct.

<400> 15
gaagcctgtg tccaggtcct tcagtgagtg gtttggcctc ggtc 44

<210> 16
<211> 1524
<212> DNA
<213> Homo sapiens

<400> 16
ggcgccgcgt aggcccgga ggccggccg gccgggctgc gagcgcctgc 50
ccatgcgcc gccgccttc cgcacgtgt tcccctcgcg gaggaaagcg 100
gcgcagctgc cctgggagga cggcaggtcc gggttgcctc ccggcggcct 150
ccctcggaag tggccgtct tccacctgtt cgtggcctgc ctctcgctgg 200
gcttcttctc cctactctgg ctgcagctca gctgctctgg ggacgtggcc 250

cgggcagtca ggggacaagg gcaggagacc tcgggcctc cccgtgcctg 300
ccccccagag ccgcggccctg agcactggga agaagacgca tcctgggccc 350
cccacccgctt ggcagtgcgt tgcccttcc gcgaacgctt cgaggagctc 400
ctggtcttcg tgcccccacat gcgcgcgttc ctgagcagga agaagatccg 450
gcaccacatc tacgtgctca accaggtgga ccacttcagg ttcaaccggg 500
cagcgctcat caacgtggc ttccctggaga gcagcaacag cacggactac 550
attgccatgc acgacgttga cctgctccct ctcaacgagg agctggacta 600
tggcttcctt gaggctggc cttccacgt ggcctccccc gagctccacc 650
ctctctacca ctacaagacc tatgtcggcg gcacccgtct gctctccaaag 700
cagcaactacc ggctgtgcaa tggatgtcc aaccgcttct gggctgggg 750
ccgcgaggac gacgagttct accggcgcat taaggagct gggctccagc 800
ttttccgccc ctcggaaatc acaactgggt acaagacatt tcgcccacctg 850
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acaggagcag ttcaagggtgg acagggaggg aggcctgaac actgtgaagt 950
accatgtggc ttcccgact gcccgtctg tggcggggc cccctgact 1000
gtcctcaaca tcatgttggc ctgtgacaag accggccacac cctggtgac 1050
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tgaacaggac aacctctcat cacccccaaa aaaaaaaaaa aaaaaaaaaa 1500
aaaaaaaaaa aaaaaaaaaa aaaa 1524

<210> 17
<211> 327
<212> PRT
<213> Homo sapiens

<220>

<221> sig_peptide
 <222> 1-42
 <223> Signal peptide.

<220>
 <221> misc_feature
 <222> 19-25,65-71,247-253,285-291,303-310
 <223> N-myristoylation site.

<220>
 <221> misc_feature
 <222> 27-31
 <223> cAMP- and cGMP-dependent protein kinase phosphorylation site.

<220>
 <221> TRANSMEM
 <222> 29-49
 <223> Transmembrane domain (type II).

<220>
 <221> misc_feature
 <222> 154-158
 <223> N-glycosylation site.

<220>
 <221> misc_feature
 <222> 226-233
 <223> Tyrosine kinase phosphorylation site.

<400> 17
 Met Phe Pro Ser Arg Arg Lys Ala Ala Gln Leu Pro Trp Glu Asp
 1 5 10 15

Gly Arg Ser Gly Leu Leu Ser Gly Gly Leu Pro Arg Lys Cys Ser
 20 25 30

Val Phe His Leu Phe Val Ala Cys Leu Ser Leu Gly Phe Phe Ser
 35 40 45

Leu Leu Trp Leu Gln Leu Ser Cys Ser Gly Asp Val Ala Arg Ala
 50 55 60

Val Arg Gly Gln Gly Gln Glu Thr Ser Gly Pro Pro Arg Ala Cys
 65 70 75

Pro Pro Glu Pro Pro Glu His Trp Glu Glu Asp Ala Ser Trp
 80 85 90

Gly Pro His Arg Leu Ala Val Leu Val Pro Phe Arg Glu Arg Phe
 95 100 105

Glu Glu Leu Leu Val Phe Val Pro His Met Arg Arg Phe Leu Ser
 110 115 120

Arg Lys Lys Ile Arg His His Ile Tyr Val Leu Asn Gln Val Asp
 125 130 135

His Phe Arg Phe Asn Arg Ala Ala Leu Ile Asn Val Gly Phe Leu

140	145	150
Glu Ser Ser Asn Ser Thr Asp Tyr Ile Ala Met His Asp Val Asp		
155	160	165
Leu Leu Pro Leu Asn Glu Glu Leu Asp Tyr Gly Phe Pro Glu Ala		
170	175	180
Gly Pro Phe His Val Ala Ser Pro Glu Leu His Pro Leu Tyr His		
185	190	195
Tyr Lys Thr Tyr Val Gly Gly Ile Leu Leu Leu Ser Lys Gln His		
200	205	210
Tyr Arg Leu Cys Asn Gly Met Ser Asn Arg Phe Trp Gly Trp Gly		
215	220	225
Arg Glu Asp Asp Glu Phe Tyr Arg Arg Ile Lys Gly Ala Gly Leu		
230	235	240
Gln Leu Phe Arg Pro Ser Gly Ile Thr Thr Gly Tyr Lys Thr Phe		
245	250	255
Arg His Leu His Asp Pro Ala Trp Arg Lys Arg Asp Gln Lys Arg		
260	265	270
Ile Ala Ala Gln Lys Gln Glu Gln Phe Lys Val Asp Arg Glu Gly		
275	280	285
Gly Leu Asn Thr Val Lys Tyr His Val Ala Ser Arg Thr Ala Leu		
290	295	300
Ser Val Gly Gly Ala Pro Cys Thr Val Leu Asn Ile Met Leu Asp		
305	310	315
Cys Asp Lys Thr Ala Thr Pro Trp Cys Thr Phe Ser		
320	325	

<210> 18
 <211> 23
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-23
 <223> Synthetic construct.

<400> 18
 gcgaacgctt cgaggagtcc tgg 23

<210> 19
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence

<222> 1-24
<223> Synthetic construct

<400> 19
gcagtgcggg aagccacatg gtac 24

<210> 20
<211> 46
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-46
<223> Synthetic construct.

<400> 20
cttcctgagc aggaagaaga tccggcacca catctacgtg ctcaac 46

<210> 21
<211> 494
<212> DNA
<213> Homo sapiens

<400> 21
caatgtttgc ctatccacct cccccaagcc cctttaccta tgctgctgct 50
aacgctgctg ctgctgctgc tgctgcttaa aggctcatgc ttggagtggg 100
gactggtcgg tgcccaagaaa gtctcttctg ccactgacgc ccccatcagg 150
gattgggcct tctttccccc ttcctttctg tgtctcctgc ctcatcgccc 200
tgccatgacc tgcagccaag cccagccccc tggggaaaggg gagaaaagtgg 250
gggatggcta agaaagctgg gagataggga acagaagagg gtagtgggtg 300
ggcttaggggg gctgccttat ttaaagtggt tgtttatgat tcttatacta 350
atttatacaa agatattaag gccctgttca ttaagaaatt gttcccttcc 400
cctgtgttca atgtttgtaa agattgttct gtgtaaatat gtctttataa 450
taaacagtta aaagctgaaa aaaaaaaaaa aaaaaaaaaa aaaa 494

<210> 22
<211> 73
<212> PRT
<213> Homo sapiens

<220>
<221> sig_peptide
<222> 1-15
<223> Signal peptide.

<220>
<221> misc_feature
<222> 3-18

<223> Growth factor and cytokines receptors family.

<400> 22

Met	Leu	Leu	Leu	Thr	Leu	Lys	Gly							
1				5				10				15		
Ser	Cys	Leu	Glu	Trp	Gly	Leu	Val	Gly	Ala	Gln	Lys	Val	Ser	Ser
					20			25			30			
Ala	Thr	Asp	Ala	Pro	Ile	Arg	Asp	Trp	Ala	Phe	Phe	Pro	Pro	Ser
					35			40			45			
Phe	Leu	Cys	Leu	Leu	Pro	His	Arg	Pro	Ala	Met	Thr	Cys	Ser	Gln
					50			55			60			
Ala	Gln	Pro	Arg	Gly	Glu	Gly	Glu	Lys	Val	Gly	Asp	Gly		
					65			70						

<210> 23

<211> 2883

<212> DNA

<213> Homo sapiens

<400> 23

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cagcggacaa aggagcatgt ccgcgcggg gaaggcccgt cctccggccg 100
ccataaggct ccggtcgccc ctgggcccgc gccgcgtcc tgcccgcccc 150
ggctccgggg cggcccgcta ggccagtgcg ccgcgcgtcg cccgcagggc 200
cccgccccgc agcatggagc cacccggacg ccggcggggc cgcgcgacgc 250
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cccaaccgca cggtcaccct gattctgagt aacaataaga tatccgagct 500
gaagaatggc tcattttctg ggttaagtct cttgaaaga ttggacacctc 550
gaaacaatct tatttagt atagatccag gtgccttctg gggactgtca 600
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cggtctttgg aattccagac tgagtatctt ttgtgtgact gtaacatact 800
gtggatgcat cgctggtaa aggagaagaa catcacggta cgggatacca 850

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gatgggagaa tagttgaaac cgatgaatcg caaggtattt ttgttggaaaa 1100
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tcatgaacgt gtcctgtggc tggcgcagag ggaagctaaa gcctgcagta 1750
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tggcagcctc tgatcgtaca ggactttcg attatggag gcgggatcca 1950
gagggaaacc tggataagca gctgagctt aagtgcataatg tttcaaatac 2000
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ccttattaaa agatttttt ttgcaggaag ataggtatta ttgcctttgc 2150
tactgtttta aagaaaaacta accaggaaga actgcattac gactttcaag 2200
ggcccttaggc attttgccct ttgattccct ttcttcacat aaaaatatca 2250
gaaattacat ttataactg cagtggata aatgcataata tactattgtt 2300

acatgtgaaa aaattttatt tgacttaaaa gtttatttat ttgtttttt 2350
gctcctgatt ttaagacaat aagatgttt catggccccc taaaagtatc 2400
atgagcctt ggcactgcgc ctgccaagcc tagtggagaa gtcaaccctg 2450
agaccaggtg tttaatcaag caagctgtat atcaaaattt ttggcagaaa 2500
acacaaatat gtcataatc ttttttaaa aaaagtattt cattgaagca 2550
agcaaaatga aagcattttt actgattttt aaaattggtg cttagatat 2600
atttgactac actgtattga agcaaataga ggaggcacaa ctccagcacc 2650
ctaatttgaac cacattttt tcacttagct ttctgtggc atgtgtatt 2700
gtattctctg cggttttaa tctcacagta cttagttct gtcttgcacc 2750
tcaataataat cacaacaat attccagtca ttttaatggc tgcataataa 2800
ctgatccaac aggtgttagg tggtctgggt tagtgtgagc actcaataaa 2850
tattgaatga atgaacgaaa aaaaaaaaaaaa aaa 2883

<210> 24
<211> 616
<212> PRT
<213> Homo sapiens

<220>
<221> sig_peptide
<222> 1-33
<223> Signal peptide.

<220>
<221> TRANSMEM
<222> 13-40
<223> Transmembrane domain (type II).

<400> 24
Met Glu Pro Pro Gly Arg Arg Arg Gly Arg Ala Gln Pro Pro Leu
1 5 10 15
Leu Leu Pro Leu Ser Leu Leu Ala Leu Leu Ala Leu Leu Gly Gly
20 25 30
Gly Gly Gly Gly Gly Ala Ala Ala Leu Pro Ala Gly Cys Lys His
35 40 45
Asp Gly Arg Pro Arg Gly Ala Gly Arg Ala Ala Gly Ala Ala Glu
50 55 60
Gly Lys Val Val Cys Ser Ser Leu Glu Leu Ala Gln Val Leu Pro
65 70 75
Pro Asp Thr Leu Pro Asn Arg Thr Val Thr Leu Ile Leu Ser Asn
80 85 90

Asn Lys Ile Ser Glu Leu Lys Asn Gly Ser Phe Ser Gly Leu Ser
 95 100 105
 Leu Leu Glu Arg Leu Asp Leu Arg Asn Asn Leu Ile Ser Ser Ile
 110 115 120
 Asp Pro Gly Ala Phe Trp Gly Leu Ser Ser Leu Lys Arg Leu Asp
 125 130 135
 Leu Thr Asn Asn Arg Ile Gly Cys Leu Asn Ala Asp Ile Phe Arg
 140 145 150
 Gly Leu Thr Asn Leu Val Arg Leu Asn Leu Ser Gly Asn Leu Phe
 155 160 165
 Ser Ser Leu Ser Gln Gly Thr Phe Asp Tyr Leu Ala Ser Leu Arg
 170 175 180
 Ser Leu Glu Phe Gln Thr Glu Tyr Leu Leu Cys Asp Cys Asn Ile
 185 190 195
 Leu Trp Met His Arg Trp Val Lys Glu Lys Asn Ile Thr Val Arg
 200 205 210
 Asp Thr Arg Cys Val Tyr Pro Lys Ser Leu Gln Ala Gln Pro Val
 215 220 225
 Thr Gly Val Lys Gln Glu Leu Leu Thr Cys Asp Pro Pro Leu Glu
 230 235 240
 Leu Pro Ser Phe Tyr Met Thr Pro Ser His Arg Gln Val Val Phe
 245 250 255
 Glu Gly Asp Ser Leu Pro Phe Gln Cys Met Ala Ser Tyr Ile Asp
 260 265 270
 Gln Asp Met Gln Val Leu Trp Tyr Gln Asp Gly Arg Ile Val Glu
 275 280 285
 Thr Asp Glu Ser Gln Gly Ile Phe Val Glu Lys Asn Met Ile His
 290 295 „ 300
 Asn Cys Ser Leu Ile Ala Ser Ala Leu Thr Ile Ser Asn Ile Gln
 305 310 315
 Ala Gly Ser Thr Gly Asn Trp Gly Cys His Val Gln Thr Lys Arg
 320 325 330
 Gly Asn Asn Thr Arg Thr Val Asp Ile Val Val Leu Glu Ser Ser
 335 340 345
 Ala Gln Tyr Cys Pro Pro Glu Arg Val Val Asn Asn Lys Gly Asp
 350 355 360
 Phe Arg Trp Pro Arg Thr Leu Ala Gly Ile Thr Ala Tyr Leu Gln
 365 370 375
 Cys Thr Arg Asn Thr His Gly Ser Gly Ile Tyr Pro Gly Asn Pro

380	385	390
Gln Asp Glu Arg Lys Ala Trp Arg Arg Cys Asp Arg Gly Gly Phe		
395	400	405
Trp Ala Asp Asp Asp Tyr Ser Arg Cys Gln Tyr Ala Asn Asp Val		
410	415	420
Thr Arg Val Leu Tyr Met Phe Asn Gln Met Pro Leu Asn Leu Thr		
425	430	435
Asn Ala Val Ala Thr Ala Arg Gln Leu Leu Ala Tyr Thr Val Glu		
440	445	450
Ala Ala Asn Phe Ser Asp Lys Met Asp Val Ile Phe Val Ala Glu		
455	460	465
Met Ile Glu Lys Phe Gly Arg Phe Thr Lys Glu Glu Lys Ser Lys		
470	475	480
Glu Leu Gly Asp Val Met Val Asp Ile Ala Ser Asn Ile Met Leu		
485	490	495
Ala Asp Glu Arg Val Leu Trp Leu Ala Gln Arg Glu Ala Lys Ala		
500	505	510
Cys Ser Arg Ile Val Gln Cys Leu Gln Arg Ile Ala Thr Tyr Arg		
515	520	525
Leu Ala Gly Gly Ala His Val Tyr Ser Thr Tyr Ser Pro Asn Ile		
530	535	540
Ala Leu Glu Ala Tyr Val Ile Lys Ser Thr Gly Phe Thr Gly Met		
545	550	555
Thr Cys Thr Val Phe Gln Lys Val Ala Ala Ser Asp Arg Thr Gly		
560	565	570
Leu Ser Asp Tyr Gly Arg Arg Asp Pro Glu Gly Asn Leu Asp Lys		
575	580	585
Gln Leu Ser Phe Lys Cys Asn Val Ser Asn Thr Phe Ser Ser Leu		
590	595	600
Ala Leu Lys Val Cys Tyr Ile Leu Gln Ser Phe Lys Thr Ile Tyr		
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Ser		

<210> 25
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24

<223> Synthetic construct

<400> 25
gaggactcac caatctgggtt cggc 24

<210> 26
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 26
aactggaaag gaaggctgtc tccc 24

<210> 27
<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 27
gtaaaaggaga agaacatcac ggtacgggat accaggtgtg tttatcctaa 50

<210> 28
<211> 683
<212> DNA
<213> Homo sapiens

<400> 28
gcgtgggat gtctaggagc tcgaagggtgg tgctggcct ctcgggtgtg 50
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gcagaggcctt cgtgacggag ttatcagaga cattgagagg caaattcgga 150
aaaaagaaaa cattcgtctt ttgggagaac agattatttt gactgagcaa 200
cttgaagcag aaagagagaa gatgttattt gcaaaaaggat ctcaaaaatc 250
atgacttcaa tgtgaaatat ctgttggaca gacaacacga gtttgtgtt 300
gtgtgttgat ggagagtagc ttagtagtat cttcatctt ttttttggtc 350
actgtccttt taaaacttgat caaataaagg acagtgggtc atataagtt 400
ctgctttcag ggtcccttat atctgaataa aggagtgtgg gcagacactt 450
tttggaaagag tctgtctggg tgatcctggt agaagccccca ttagggtcac 500
tgtccagtgc ttagggttgt tactgagaag cactgcccag cttgtgagaa 550

ggaaggatg gatagtagca tccacctgag tagtctgatc agtcggcatg 600
atgacgaagc cacgagaaca tcgacctcag aaggactgga ggaaggtgaa 650
gtggagggag agacgctcct gatcgctgaa tcc 683

<210> 29
<211> 81
<212> PRT
<213> Homo sapiens

<220>
<221> sig_peptide
<222> 1-21
<223> Signal peptide.

<400> 29
Met Ser Arg Ser Ser Lys Val Val Leu Gly Leu Ser Val Leu Leu
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Thr Ala Ala Thr Val Ala Gly Val His Val Lys Gln Gln Trp Asp
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Gln Gln Arg Leu Arg Asp Gly Val Ile Arg Asp Ile Glu Arg Gln
35 40 45

Ile Arg Lys Lys Glu Asn Ile Arg Leu Leu Gly Glu Gln Ile Ile
50 55 60

Leu Thr Glu Gln Leu Glu Ala Glu Arg Glu Lys Met Leu Leu Ala
65 70 75

Lys Gly Ser Gln Lys Ser
80

<210> 30
<211> 2128
<212> DNA
<213> Homo sapiens

<400> 30
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tccgtggatt cctctgctaa gaccgctgcc atgccagtga cggttaacccg 150
caccaccatc acaaccacca cgacgtcatc ttcgggcctg gggccccca 200
tgatcggtgg gtcccccctcg gcccctgacac agcccccgtgg tctccctcgc 250
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<210> 31
<211> 322
<212> PRT
<213> Homo sapiens

<400> 31
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Ala Leu Thr Gln Pro Leu Gly Leu Leu Arg Leu Leu Gln Leu Val
35 40 45
Ser Thr Cys Val Ala Phe Ser Leu Val Ala Ser Val Gly Ala Trp
50 55 60
Thr Gly Ser Met Gly Asn Trp Ser Met Phe Thr Trp Cys Phe Cys
65 70 75
Phe Ser Val Thr Leu Ile Ile Leu Ile Val Glu Leu Cys Gly Leu
80 85 90
Gln Ala Arg Phe Pro Leu Ser Trp Arg Asn Phe Pro Ile Thr Phe
95 100 105
Ala Cys Tyr Ala Ala Leu Phe Cys Leu Ser Ala Ser Ile Ile Tyr
110 115 120
Pro Thr Thr Tyr Val Gln Phe Leu Ser His Gly Arg Ser Arg Asp
125 130 135
His Ala Ile Ala Ala Thr Phe Ser Cys Ile Ala Cys Val Ala
140 145 150
Tyr Ala Thr Glu Val Ala Trp Thr Arg Ala Arg Pro Gly Glu Ile
155 160 165
Thr Gly Tyr Met Ala Thr Val Pro Gly Leu Leu Lys Val Leu Glu
170 175 180
Thr Phe Val Ala Cys Ile Ile Phe Ala Phe Ile Ser Asp Pro Asn
185 190 195
Leu Tyr Gln His Gln Pro Ala Leu Glu Trp Cys Val Ala Val Tyr
200 205 210

Ala Ile Cys Phe Ile Leu Ala Ala Ile Ala Ile Leu Leu Asn Leu
 215 220 225

Gly Glu Cys Thr Asn Val Leu Pro Ile Pro Phe Pro Ser Phe Leu
 230 235 240

Ser Gly Leu Ala Leu Leu Ser Val Leu Leu Tyr Ala Thr Ala Leu
 245 250 255

Val Leu Trp Pro Leu Tyr Gln Phe Asp Glu Lys Tyr Gly Gly Gln
 260 265 270

Pro Arg Arg Ser Arg Asp Val Ser Cys Ser Arg Ser His Ala Tyr
 275 280 285

Tyr Val Cys Ala Trp Asp Arg Arg Leu Ala Val Ala Ile Leu Thr
 290 295 300

Ala Ile Asn Leu Leu Ala Tyr Val Ala Asp Leu Val His Ser Ala
 305 310 315

His Leu Val Phe Val Lys Val
 320

<210> 32
<211> 3680
<212> DNA
<213> *Homo sapiens*

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ctggccagcc tatgcatttt taagaaatta ttctgttatta ggtgctgtgc 200
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ttattactca ctatgactaa gggtcacaaa tggggtacgt tcatggagag 350
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gcccaaggta agaacgagag ccaacggca caagcattct atatataagt 3600

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 taatataaaa atcttggtaa atctctaaaa 3680
 <210> 33
 <211> 335
 <212> PRT
 <213> Homo sapiens
 <400> 33
 Met Phe Leu Ala Thr Leu Ser Phe Leu Leu Pro Phe Ala His Pro
 1 5 10 15
 Phe Gly Thr Val Ser Cys Glu Tyr Met Leu Gly Ser Pro Leu Ser
 20 25 30
 Ser Leu Ala Gln Val Asn Leu Ser Pro Phe Ser His Pro Lys Val
 35 40 45
 His Met Asp Pro Asn Tyr Cys His Pro Ser Thr Ser Leu His Leu
 50 55 60
 Cys Ser Leu Ala Trp Ser Phe Thr Arg Leu Leu His Pro Pro Leu
 65 70 75
 Ser Pro Gly Ile Ser Gln Val Val Lys Asp His Val Thr Lys Pro
 80 85 90
 Thr Ala Met Ala Gln Gly Arg Val Ala His Leu Ile Glu Trp Lys
 95 100 105
 Gly Trp Ser Lys Pro Ser Asp Ser Pro Ala Ala Leu Glu Ser Ala
 110 115 120
 Phe Ser Ser Tyr Ser Asp Leu Ser Glu Gly Glu Gln Glu Ala Arg
 125 130 135
 Phe Ala Ala Gly Val Ala Glu Gln Phe Ala Ile Ala Glu Ala Lys
 140 145 150
 Leu Arg Ala Trp Ser Ser Val Asp Gly Glu Asp Ser Thr Asp Asp
 155 160 165
 Ser Tyr Asp Glu Asp Phe Ala Gly Gly Met Asp Thr Asp Met Ala
 170 175 180
 Gly Gln Leu Pro Leu Gly Pro His Leu Gln Asp Leu Phe Thr Gly
 185 190 195
 His Arg Phe Ser Arg Pro Val Arg Gln Gly Ser Val Glu Pro Glu
 200 205 210
 Ser Asp Cys Ser Gln Thr Val Ser Pro Asp Thr Leu Cys Ser Ser
 215 220 225
 Leu Cys Ser Leu Glu Asp Gly Leu Leu Gly Ser Pro Ala Arg Leu
 230 235 240

Ala Ser Gln Leu Leu Gly Asp Glu Leu Leu Leu Ala Lys Leu Pro
245 250 255

Pro Ser Arg Glu Ser Ala Phe Arg Ser Leu Gly Pro Leu Glu Ala
260 265 270

Gln Asp Ser Leu Tyr Asn Ser Pro Leu Thr Glu Ser Cys Leu Ser
275 280 285

Pro Ala Glu Glu Glu Pro Ala Pro Cys Lys Asp Cys Gln Pro Leu
290 295 300

Cys Pro Pro Leu Thr Gly Ser Trp Glu Arg Gln Arg Gln Ala Ser
305 310 315

Asp Leu Ala Ser Ser Gly Val Val Ser Leu Asp Glu Asp Glu Ala
320 325 330

Glu Pro Glu Glu Gln
335

<210> 34
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-25
<223> Synthetic construct

<400> 34
tgtcctttgt cccagacttc tgtcc 25

<210> 35
<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 35
ctggatgcta atgtgtccag taaatgatcc ccttatcccg tcgcgatgct 50

<210> 36
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-25
<223> Synthetic construct.

<400> 36

ttccactcaa tgaggtgagc cactc 25

<210> 37
<211> 23
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-23
<223> Synthetic construct.

<400> 37
ggcgagccct aactatccag gag 23

<210> 38
<211> 39
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-39
<223> Synthetic construct.

<400> 38
ggagatcgct gcgctggcca ggtcctccct gcatggat 39

<210> 39
<211> 22
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-22
<223> Synthetic construct.

<400> 39
ctgctgcaaa gcgagcctct tg 22

<210> 40
<211> 2084
<212> DNA
<213> Homo sapiens

<400> 40
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tttggtttcc ctggcacccct cctgctcagt ggcacattgt cacacttaac 100
ccatctgttt tctctaattgc acgacagatt ccttcagac aggacaactg 150
tgatatttca gttccctgatt gtaaataacct cctaagcctg aagcttctgt 200
tactagccat tgtgagcttc agtttcttca tctgcaaaat gggcataata 250
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aataccaaag aagcctacaa tggtggcctt agccaaattt ctgttgattt 350
caacgttgtt ttattcactt ctatcgggaa gccatggaaa agaaaatcaa 400
gacataaaca caacacagaa cattgcagaa gtttttaaaa caatggaaaa 450
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gcaagtgtca tctacatcct agcctttga caaattcatc tttcaaaagg 1400
ttacacaaaa ttactgtcac gtggattttg tcaaggagaa tcataaaagc 1450
aggagaccag tagcagaaat gtagacagga tgtatcatcc aaaggtttc 1500
tttcttacaa ttttggcca tcctgaggca tttactaagt agccttaatt 1550
tgtatTTTGTAG tagtattttc ttagtagaaa atatttggg aatcagataa 1600
aactaaaaaga ttccaccatt acagccctgc ctcataacta aataataaaa 1650
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catagcccaag agtttctgtt attggaaat tgaggcaata gaaatgacag 1850
acctgtattc tagtacgtta taattttcta gatcagcaca cacatgatca 1900
gcccactgag ttatgaagct gacaatgact gcattcaacg gggccatggc 1950
aggaaagctg accctaccca ggaaagtaat agttcttta aaagtcttca 2000
aaggtttgg gaatttaac ttgtcttaat atatcttagg cttcaattat 2050
ttgggtgcct taaaaactca atgagaatca tgg 2084

<210> 41

<211> 334

<212> PRT

<213> Homo sapiens

<400> 41

Met Leu Ala Leu Ala Lys Ile Leu Leu Ile Ser Thr Leu Phe Tyr
1 5 10 15

Ser Leu Leu Ser Gly Ser His Gly Lys Glu Asn Gln Asp Ile Asn
20 25 30

Thr Thr Gln Asn Ile Ala Glu Val Phe Lys Thr Met Glu Asn Lys
35 40 45

Pro Ile Ser Leu Glu Ser Glu Ala Asn Leu Asn Ser Asp Lys Glu
50 55 60

Asn Ile Thr Thr Ser Asn Leu Lys Ala Ser His Ser Pro Pro Leu
65 70 75

Asn Leu Pro Asn Asn Ser His Gly Ile Thr Asp Phe Ser Ser Asn
80 85 90

Ser Ser Ala Glu His Ser Leu Gly Ser Leu Lys Pro Thr Ser Thr
95 100 105

Ile Ser Thr Ser Pro Pro Leu Ile His Ser Phe Val Ser Lys Val
110 115 120

Pro Trp Asn Ala Pro Ile Ala Asp Glu Asp Leu Leu Pro Ile Ser
125 130 135

Ala His Pro Asn Ala Thr Pro Ala Leu Ser Ser Glu Asn Phe Thr
140 145 150

Trp Ser Leu Val Asn Asp Thr Val Lys Thr Pro Asp Asn Ser Ser
155 160 165

Ile Thr Val Ser Ile Leu Ser Ser Glu Pro Thr Ser Pro Ser Val
170 175 180

Thr Pro Leu Ile Val Glu Pro Ser Gly Trp Leu Thr Thr Asn Ser
185 190 195

Asp	Ser	Phe	Thr	Gly	Phe	Thr	Pro	Tyr	Gln	Glu	Lys	Thr	Thr	Leu
200							205						210	
Gln	Pro	Thr	Leu	Lys	Phe	Thr	Asn	Asn	Ser	Lys	Leu	Phe	Pro	Asn
215							220						225	
Thr	Ser	Asp	Pro	Gln	Lys	Glu	Asn	Arg	Asn	Thr	Gly	Ile	Val	Phe
230							235					240		
Gly	Ala	Ile	Leu	Gly	Ala	Ile	Leu	Gly	Val	Ser	Leu	Leu	Thr	Leu
245							250					255		
Val	Gly	Tyr	Leu	Leu	Cys	Gly	Lys	Arg	Lys	Thr	Asp	Ser	Phe	Ser
260							265					270		
His	Arg	Arg	Leu	Tyr	Asp	Asp	Arg	Asn	Glu	Pro	Val	Leu	Arg	Leu
275							280					285		
Asp	Asn	Ala	Pro	Glu	Pro	Tyr	Asp	Val	Ser	Phe	Gly	Asn	Ser	Ser
290							295					300		
Tyr	Tyr	Asn	Pro	Thr	Leu	Asn	Asp	Ser	Ala	Met	Pro	Glu	Ser	Glu
305							310					315		
Glu	Asn	Ala	Arg	Asp	Gly	Ile	Pro	Met	Asp	Asp	Ile	Pro	Pro	Leu
320							325					330		
Arg Thr Ser Val														

<210> 42
 <211> 1594
 <212> DNA
 <213> Homo sapiens

<400> 42
 aacaggatct cctcttgcag tctgcagccc aggacgctga ttccagcagc 50
 gccttaccgc gcagcccgaa gattcactat ggtgaaaatc gccttcaata 100
 ccccttaccgc cgtgcaaaag gaggaggcgc ggcaaga<gt> ggaggccctc 150
 ctgagccgca cggtcagaac tcagatactg accggcaagg agctccgagt 200
 tgccacccag gaaaaagagg gtcctctgg gagatgtatg cttactct 250
 taggccttc attcatcttgcaggactta ttgttggtgg agcctgcatt 300
 tacaagtact tcatgccaa gagcaccatt taccgtggag agatgtgctt 350
 ttttgattct gaggatcctg caaattccct tcgtggagga gagcctaact 400
 tcctgcctgt gactgaggag gctgacattc gtgaggatga caacattgca 450
 atcattgtatg tgcctgtccc cagttctct gatagtgacc ctgcagcaat 500
 tattcatgac tttgaaaaagg gaatgactgc ttacctggac ttgttgcctgg 550

ggaactgcta tctgatgccc ctcataactt ctattgttat gcctccaaaa 600
aatctggtag agctcttgg caaactggcg agtggcagat atctgcctca 650
aacttatgtg gttcgagaag acctagttgc tgtggaggaa attcgtgatg 700
ttagtaacct tggcatctt atttaccaac tttgcaataa cagaaagtcc 750
ttccgccttc gtcgcagaga cctcttgctg ggttcaaca aacgtgccat 800
tgataaatgc tggaagatta gacacttccc caacgaattt attgttggaga 850
ccaagatctg tcaagagtaa gaggcaacag atagagtgtc cttggtaata 900
agaagtcaga gatttacaat atgacttaa cattaagggtt tatgggatac 950
tcaagatatt tactcatgca tttactctat tgctttagtct taaaaaaaaag 1000
aaaaaaaaaaa aaaactacta accactgcaa gctcttgtca aatttttagtt 1050
taattggcat tgcttggtt ttgaaactga aattacatga gtttcatttt 1100
ttcttgcat ttatagggtt tagatttctg aaagcagcat gaatatatca 1150
cctaacatcc tgacaataaa ttccatccgt tgttttttt gtttgggtt 1200
ttttctttt ccttaagta agctctttt tcattttatg gtggagcaat 1250
tttaaaattt gaaatatttt aaattgtttt tgaactttt gtgtaaaata 1300
tatcagatct caacattgtt gtttctttt gttttcatt ttgtacaact 1350
ttcttgaatt tagaaattac atctttgcag ttctgttagg tgctctgtaa 1400
ttaacctgac ttatatgtga acaattttca tgagacagtc attttaact 1450
aatgcagtga ttcttctca ctactatctg tattgtggaa tgcacaaaaat 1500
tgtgttaggtg ctgaatgctg taaggagttt aggttgtatg aattctacaa 1550
ccctataata aattttactc tataaaaaaa aaaaaaaaaa aaaa 1594

<210> 43

<211> 263

<212> PRT

<213> Homo sapiens

<400> 43

Met Val Lys Ile Ala Phe Asn Thr Pro Thr Ala Val Gln Lys Glu
1 5 10 15

Glu Ala Arg Gln Asp Val Glu Ala Leu Leu Ser Arg Thr Val Arg
20 25 30

Thr Gln Ile Leu Thr Gly Lys Glu Leu Arg Val Ala Thr Gln Glu
35 40 45

Lys Glu Gly Ser Ser Gly Arg Cys Met Leu Thr Leu Leu Gly Leu

50	55	60
Ser Phe Ile Leu Ala Gly Leu Ile Val Gly Gly Ala Cys Ile Tyr		
65	70	75
Lys Tyr Phe Met Pro Lys Ser Thr Ile Tyr Arg Gly Glu Met Cys		
80	85	90
Phe Phe Asp Ser Glu Asp Pro Ala Asn Ser Leu Arg Gly Gly Glu		
95	100	105
Pro Asn Phe Leu Pro Val Thr Glu Glu Ala Asp Ile Arg Glu Asp		
110	115	120
Asp Asn Ile Ala Ile Ile Asp Val Pro Val Pro Ser Phe Ser Asp		
125	130	135
Ser Asp Pro Ala Ala Ile Ile His Asp Phe Glu Lys Gly Met Thr		
140	145	150
Ala Tyr Leu Asp Leu Leu Leu Gly Asn Cys Tyr Leu Met Pro Leu		
155	160	165
Asn Thr Ser Ile Val Met Pro Pro Lys Asn Leu Val Glu Leu Phe		
170	175	180
Gly Lys Leu Ala Ser Gly Arg Tyr Leu Pro Gln Thr Tyr Val Val		
185	190	195
Arg Glu Asp Leu Val Ala Val Glu Glu Ile Arg Asp Val Ser Asn		
200	205	210
Leu Gly Ile Phe Ile Tyr Gln Leu Cys Asn Asn Arg Lys Ser Phe		
215	220	225
Arg Leu Arg Arg Arg Asp Leu Leu Leu Gly Phe Asn Lys Arg Ala		
230	235	240
Ile Asp Lys Cys Trp Lys Ile Arg His Phe Pro Asn Glu Phe Ile		
245	250	255
Val Glu Thr Lys Ile Cys Gln Glu		
260		

<210> 44
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 44
 gaaagacacg acacagcagc ttgc 24

<210> 45

<211> 20
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-20
<223> Synthetic construct.

<400> 45
gggaactgct atctgatgcc 20

<210> 46
<211> 26
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-26
<223> Synthetic construct.

<400> 46
caggatctcc tcttgagtc tgcagc 26

<210> 47
<211> 28
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-28
<223> Synthetic construct.

<400> 47
cttctcgaac cacataagtt tgaggcag 28

<210> 48
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-25
<223> Synthetic construct.

<400> 48
cacgattccc tccacagcaa ctggg 25

<210> 49
<211> 1969
<212> DNA
<213> Homo sapiens

<400> 49
ggaggaggga gggcgggcag ggcgcagccc agagcagccc cgggcaccag 50

cacggactct ctcttccagc ccaggtgccc cccactctcg ctccattcgg 100
cgggagcacc cagtccctgta cgccaaggaa ctggctctgg gggcaccatg 150
gttccggcgg cagccccag cctcctcatc cttctgttgc tgctgctggg 200
gtctgtgcct gctaccgacg cccgctctgt gcccctgaag gccacgttcc 250
tggaggatgt ggcgggtagt ggggaggccg agggctcgtc ggcctcctcc 300
ccgagcctcc cgccaccctg gaccccgcc ctcagccca catcgatggg 350
gccccagccc acaaccctgg ggggcccattc accccccacc aacttcctgg 400
atgggatagt ggacttcttc cgccagtacg ttagtgcgtat tgctgtggg 450
ggctccctgg ctttctgct gatgttcatc gtctgtgccg cggtcatcac 500
ccggcagaag cagaaggcct cggcctattt cccatcgatcc ttcccaaga 550
agaagtacgt ggaccagagt gaccgggccg ggggcccccg ggccttcagt 600
gaggtccccg acagagcccc cgacagcagg cccgaggaag ccctggattc 650
ctcccgccag ctccaggccg acatcttggc cgccaccctag aacctcaagt 700
cccccaccag ggctgcactg ggccgtgggg acggagccag gatggtggag 750
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agtccagggaa catggggtcc cagtggagac accagaggcg caggaggagc 850
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ccccccaaagt gctgggatta caggcgtgag ccaccgtgcc cggcccaaacc 1350
tactttttaa aacagctaca gggtaaaatc ctgcagcacc cactctggaa 1400
aatactgctc ttaattttcc tgaaggtggc cccctgttcc tagttggtcc 1450
aggatttaggg atgtggggta tagggcattt aaatcctctc aagcgctctc 1500

caagcacccc cggcctgggg gtgagttct catcccgcta ctgctgctgg 1550
gatcaggttg aatgaatgga actcttcctg tctggcctcc aaagcagcct 1600
agaagctgag gggctgtgtt tgaggggacc tccaccctgg ggaagtccga 1650
ggggctgggg aagggttct gacgcccagc ctggagcagg ggggcccctgg 1700
ccacccctg ttgctcacac attgtctggc agcctgtgtc cacaatattc 1750
gtcagtcctc gacagggagc ctgggctccg tcctgcttta gggaggctct 1800
ggcaggaggt cctctcccccc atccctccat ctggggctcc cccaacctct 1850
gcacagctct ccaggtgctg agatataatg caccagcaca ataaaccttt 1900
attccggcct gaaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa 1950
aaaaaaaaaaa aaaaaaaaga 1969

<210> 50
<211> 283
<212> PRT
<213> Homo sapiens

<400> 50
Met Val Ser Ala Ala Ala Pro Ser Leu Leu Ile Leu Leu Leu Leu
1 5 10 15
Leu Leu Gly Ser Val Pro Ala Thr Asp Ala Arg Ser Val Pro Leu
20 25 30
Lys Ala Thr Phe Leu Glu Asp Val Ala Gly Ser Gly Glu Ala Glu
35 40 45
Gly Ser Ser Ala Ser Ser Pro Ser Leu Pro Pro Pro Trp Thr Pro
50 55 60
Ala Leu Ser Pro Thr Ser Met Gly Pro Gln Pro Thr Thr Leu Gly
65 70 75
Gly Pro Ser Pro Pro Thr Asn Phe Leu Asp Gly Ile Val Asp Phe
80 85 90
Phe Arg Gln Tyr Val Met Leu Ile Ala Val Val Gly Ser Leu Ala
95 100 105
Phe Leu Leu Met Phe Ile Val Cys Ala Ala Val Ile Thr Arg Gln
110 115 120
Lys Gln Lys Ala Ser Ala Tyr Tyr Pro Ser Ser Phe Pro Lys Lys
125 130 135
Lys Tyr Val Asp Gln Ser Asp Arg Ala Gly Gly Pro Arg Ala Phe
140 145 150
Ser Glu Val Pro Asp Arg Ala Pro Asp Ser Arg Pro Glu Glu Ala
155 160 165

Leu Asp Ser Ser Arg Gln Leu Gln Ala Asp Ile Leu Ala Ala Thr
170 175 180
Gln Asn Leu Lys Ser Pro Thr Arg Ala Ala Leu Gly Gly Gly Asp
185 190 195
Gly Ala Arg Met Val Glu Gly Arg Gly Ala Glu Glu Glu Lys
200 205 210
Gly Ser Gln Glu Gly Asp Gln Glu Val Gln Gly His Gly Val Pro
215 220 225
Val Glu Thr Pro Glu Ala Gln Glu Glu Pro Cys Ser Gly Val Leu
230 235 240
Glu Gly Ala Val Val Ala Gly Glu Gly Gln Gly Glu Leu Glu Gly
245 250 255
Ser Leu Leu Leu Ala Gln Glu Ala Gln Gly Pro Val Gly Pro Pro
260 265 270
Glu Ser Pro Cys Ala Cys Ser Ser Val His Pro Ser Val
275 280

<210> 51
<211> 1734
<212> DNA
<213> Homo sapiens

<400> 51
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gaccaggagg gagggaggac agggagtcgg aaggaggagg acagaggagg 100
gcacagagac gcagagcaag ggcggcaagg aggagaccct ggtgggagga 150
agacactctg gagagagagg gggctggca gagatgaagt tccaggggcc 200
cctggcctgc ctcctgctgg ccctctgcct gggcagtggg gaggctggcc 250
ccctgcagag cggagaggaa agcactggga caaatatgg ggaggccctt 300
ggacatggcc tgggagacgc cctgagcgaa ggggtggaa aggccattgg 350
caaagaggcc ggagggcag ctggctctaa agtcagttag gcccattggcc 400
aaggaccag agaagcagtt ggcactggag tcaggcaggt tccaggcttt 450
ggcgcagcag atgcattggg caacagggtc gggaaagcag cccatgcct 500
ggaaacact gggcacgaga ttggcagaca ggcagaagat gtcattcgac 550
acggagcaga tgctgtccgc ggctcctggc aggggtgcc tggccacagt 600
ggtgcttggg aaacttctgg aggcattggc atctttggct ctcaaggtagg 650
ccttggaggc cagggccagg gcaatcctgg aggtctgggg actccgtggg 700

tccacggata ccccgaaac tcagcaggca gcttggaaat gaatcctcag 750
ggagctccct ggggtcaagg aggcaatgg aggccaccaa actttggac 800
caacactcag ggagctgtgg cccagcctgg ctatggtca gtgagagcca 850
gcaaccagaa tgaagggtgc acgaatcccc caccatctgg ctcaggtgga 900
ggctccagca actctgggg aggcaagcgc tcacagtcgg gcagcagtgg 950
cagtggcagc aatggtgaca acaacaatgg cagcagcagt ggtggcagca 1000
gcagtggcag cagcagtggc agcagcagtgc gcggcagcag tggcggcagc 1050
agtggtgca gcagtggcaa cagtggtggc agcagaggtg acagcggcag 1100
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gaagcccgcg ggagcggggaa atctgggatt cagggcttca gaggacaggg 1250
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gtttcatcaa ctggatgcc ataaacaagg accagagaag ctctcgcatc 1500
ccgtgacctc cagacaagga gccaccagat tggatggag ccccccacact 1550
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aaataaacct tagctgcccc aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1650
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1700
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1734

<210> 52
<211> 440
<212> PRT
<213> Homo sapiens

<400> 52
Met Lys Phe Gln Gly Pro Leu Ala Cys Leu Leu Leu Ala Leu Cys
1 5 10 15
Leu Gly Ser Gly Glu Ala Gly Pro Leu Gln Ser Gly Glu Glu Ser
20 25 30
Thr Gly Thr Asn Ile Gly Glu Ala Leu Gly His Gly Leu Gly Asp
35 40 45
Ala Leu Ser Glu Gly Val Gly Lys Ala Ile Gly Lys Glu Ala Gly

50	55	60
Gly Ala Ala Gly Ser Lys Val Ser Glu Ala Leu Gly Gln Gly Thr		
65	70	75
Arg Glu Ala Val Gly Thr Gly Val Arg Gln Val Pro Gly Phe Gly		
80	85	90
Ala Ala Asp Ala Leu Gly Asn Arg Val Gly Glu Ala Ala His Ala		
95	100	105
Leu Gly Asn Thr Gly His Glu Ile Gly Arg Gln Ala Glu Asp Val		
110	115	120
Ile Arg His Gly Ala Asp Ala Val Arg Gly Ser Trp Gln Gly Val		
125	130	135
Pro Gly His Ser Gly Ala Trp Glu Thr Ser Gly Gly His Gly Ile		
140	145	150
Phe Gly Ser Gln Gly Gly Leu Gly Gly Gln Gly Gln Gly Asn Pro		
155	160	165
Gly Gly Leu Gly Thr Pro Trp Val His Gly Tyr Pro Gly Asn Ser		
170	175	180
Ala Gly Ser Phe Gly Met Asn Pro Gln Gly Ala Pro Trp Gly Gln		
185	190	195
Gly Gly Asn Gly Gly Pro Pro Asn Phe Gly Thr Asn Thr Gln Gly		
200	205	210
Ala Val Ala Gln Pro Gly Tyr Gly Ser Val Arg Ala Ser Asn Gln		
215	220	225
Asn Glu Gly Cys Thr Asn Pro Pro Pro Ser Gly Ser Gly Gly Gly		
230	235	240
Ser Ser Asn Ser Gly Gly Ser Gly Ser Gln Ser Gly Ser Ser		
245	250	255
Gly Ser Gly Ser Asn Gly Asp Asn Asn Asn Gly Ser Ser Ser Gly		
260	265	270
Gly Ser Ser Ser Gly Ser Ser Ser Gly Ser Ser Ser Gly Gly Ser		
275	280	285
Ser Gly Gly Ser Ser Gly Ser Ser Gly Asn Ser Gly Gly Ser		
290	295	300
Arg Gly Asp Ser Gly Ser Glu Ser Ser Trp Gly Ser Ser Thr Gly		
305	310	315
Ser Ser Ser Gly Asn His Gly Gly Ser Gly Gly Gly Asn Gly His		
320	325	330
Lys Pro Gly Cys Glu Lys Pro Gly Asn Glu Ala Arg Gly Ser Gly		
335	340	345

Glu Ser Gly Ile Gln Gly Phe Arg Gly Gln Gly Val Ser Ser Asn
350 355 360
Met Arg Glu Ile Ser Lys Glu Gly Asn Arg Leu Leu Gly Gly Ser
365 370 375
Gly Asp Asn Tyr Arg Gly Gln Gly Ser Ser Trp Gly Ser Gly Gly
380 385 390
Gly Asp Ala Val Gly Gly Val Asn Thr Val Asn Ser Glu Thr Ser
395 400 405
Pro Gly Met Phe Asn Phe Asp Thr Phe Trp Lys Asn Phe Lys Ser
410 415 420
Lys Leu Gly Phe Ile Asn Trp Asp Ala Ile Asn Lys Asp Gln Arg
425 430 435
Ser Ser Arg Ile Pro
440

<210> 53

<211> 3580

<212> DNA

<213> Homo sapiens

<400> 53

gaccgggtccc tccgggtcctg gatgtgcgga ctctgctgca gcgagggtcg 50
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ctttgctgac catgttgttc ctttgctgga atattaccgg gacatcttca 150
ctctcctgct gcgcctgcac cggagcttgg tgggtcgca ggagagttag 200
ggaaagatgt gtttcctgaa caagctgctg ctacttgctg tcctgggtcg 250
gcttttccag attcccacag tccctgagga cttgttcttt ctggaaagagg 300
gtccctcata tgcctttgag gtggacacag tagccccaga gcatggcttg 350
gacaatgcgc ctgtgggtgga ccagcagctg ctctacaccc gctgccccta 400
catcgagag ctccggaaac tgctcgcttc gtgggtgtca ggcagtagtg 450
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atcctagagg aaggagagtt ggcctgattt gggattatgg cagaaaagtc 1850
cagagatgcc agtcctggag tagaagaggt ggtgtttgtt tatctcttgg 1900
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catttgctat cccagcatct cttaaaactt tgttagtcttg gaattcatga 2000
cagaggcaaa tgactcctgc ttaacttatg aagaaagtta aaacatgaat 2050
cttgggagtc tacattttct tattcaccagg agctggactg ccatctcctt 2100
ataaaatgcct aacacaggcc gggctgggt gctcatgcct gtaatcccag 2150
cactttgaga ggcctgaggt cggcggactg cctgaggtca ggaattcaag 2200
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<210> 54
<211> 280
<212> PRT
<213> Homo sapiens

<400> 54

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Trp	Val	Ser	Gly	Ser	Ser	Gly	Arg	Ser	Gly	Gly	Phe	Met	Arg	Lys
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Ile	Thr	Pro	Thr	Thr	Thr	Ser	Leu	Gly	Ala	Gln	Pro	Ser	Gln	
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Thr	Ser	Gln	Gly	Leu	Gln	Ala	Gln	Leu	Ala	Gln	Ala	Phe	Phe	His
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Asn	Gln	Pro	Pro	Ser	Leu	Arg	Arg	Thr	Val	Glu	Phe	Val	Ala	Glu
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				200				205					210	
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				215				220					225	
Glu	Asn	Ile	Ala	Val	Gly	Leu	Ala	Thr	Glu	Lys	Ala	Cys	Ala	Trp
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Leu	Ser	Ala	Asn	Ile	Thr	Ala	Leu	Ile	Arg	Arg	Glu	Val	Lys	Ala
				245				250					255	
Ala	Val	Ser	Arg	Thr	Leu	Arg	Ala	Gln	Gly	Pro	Glu	Pro	Ala	Ala
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<211> 2401
<212> DNA
<213> Homo sapiens

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<210> 56
<211> 299
<212> PRT
<213> Homo sapiens

<400> 56
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Ile	Leu	Gly	Asn	Lys	Thr	Leu	Pro	Ser	Arg	Cys	His	Gln	Cys	Val
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Ile	Val	Ser	Ser	Ser	Ser	His	Leu	Leu	Gly	Thr	Lys	Leu	Gly	Pro
80								85					90	
Glu	Ile	Glu	Arg	Ala	Glu	Cys	Thr	Ile	Arg	Met	Asn	Asp	Ala	Pro
95								100					105	
Thr	Thr	Gly	Tyr	Ser	Ala	Asp	Val	Gly	Asn	Lys	Thr	Thr	Tyr	Arg
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185								190					195	
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245								250					255	
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<211> 4277

<212> DNA

<213> Homo sapiens

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<210> 58
<211> 1115

<212> PRT

<213> Homo sapiens

<400> 58

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			80					85				90		
Leu	Val	Ile	Thr	Ala	Leu	Asn	Asn	His	Thr	Val	Gly	Arg	Tyr	Gln
			95					100				105		
Cys	Val	Ala	Arg	Met	Pro	Ala	Gly	Ala	Val	Ala	Ser	Val	Pro	Ala
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Thr	Val	Thr	Leu	Ala	Asn	Leu	Gln	Asp	Phe	Lys	Leu	Asp	Val	Gln
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 320 325 330
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 335 340 345
 Val Arg Gly Asn Pro Pro Pro Ser Val Leu Trp Leu Arg Asn Ala
 350 355 360
 Val Pro Leu Ile Ser Ser Gln Arg Leu Arg Leu Ser Arg Arg Ala
 365 370 375
 Leu Arg Val Leu Ser Met Gly Pro Glu Asp Glu Gly Val Tyr Gln
 380 385 390
 Cys Met Ala Glu Asn Glu Val Gly Ser Ala His Ala Val Val Gln
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 410 415 420
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 Gly Asn Pro Glu Gln Met Leu Arg Gly Gln Pro Ala Leu Pro Arg
 440 445 450
 Pro Pro Thr Ser Val Gly Pro Ala Ser Pro Lys Cys Pro Gly Glu
 455 460 465
 Lys Gly Gln Gly Ala Pro Ala Glu Ala Pro Ile Ile Leu Ser Ser
 470 475 480
 Pro Arg Thr Ser Lys Thr Asp Ser Tyr Glu Leu Val Trp Arg Pro
 485 490 495
 Arg His Glu Gly Ser Gly Arg Ala Pro Ile Leu Tyr Tyr Val Val
 500 505 510
 Lys His Arg Lys Gln Val Thr Asn Ser Ser Asp Asp Trp Thr Ile
 515 520 525
 Ser Gly Ile Pro Ala Asn Gln His Arg Leu Thr Leu Thr Arg Leu
 530 535 540
 Asp Pro Gly Ser Leu Tyr Glu Val Glu Met Ala Ala Tyr Asn Cys
 545 550 555
 Ala Gly Glu Gly Gln Thr Ala Met Val Thr Phe Arg Thr Gly Arg

560	565	570
Arg Pro Lys Pro Glu Ile Met Ala Ser Lys	Glu Gln Gln Ile Gln	
575	580	585
Arg Asp Asp Pro Gly Ala Ser Pro Gln Ser	Ser Ser Ser Gln Pro Asp	
590	595	600
His Gly Arg Leu Ser Pro Pro Glu Ala Pro	Asp Arg Pro Thr Ile	
605	610	615
Ser Thr Ala Ser Glu Thr Ser Val Tyr Val	Thr Trp Ile Pro Arg	
620	625	630
Gly Asn Gly Gly Phe Pro Ile Gln Ser Phe	Arg Val Glu Tyr Lys	
635	640	645
Lys Leu Lys Lys Val Gly Asp Trp Ile Leu	Ala Thr Ser Ala Ile	
650	655	660
Pro Pro Ser Arg Leu Ser Val Glu Ile Thr	Gly Leu Glu Lys Gly	
665	670	675
Thr Ser Tyr Lys Phe Arg Val Arg Ala Leu	Asn Met Leu Gly Glu	
680	685	690
Ser Glu Pro Ser Ala Pro Ser Arg Pro Tyr	Val Val Ser Gly Tyr	
695	700	705
Ser Gly Arg Val Tyr Glu Arg Pro Val Ala	Gly Pro Tyr Ile Thr	
710	715	720
Phe Thr Asp Ala Val Asn Glu Thr Thr Ile	Met Leu Lys Trp Met	
725	730	735
Tyr Ile Pro Ala Ser Asn Asn Asn Thr Pro	Ile His Gly Phe Tyr	
740	745	750
Ile Tyr Tyr Arg Pro Thr Asp Ser Asp Asn	Asp Ser Asp Tyr Lys	
755	760	765
Lys Asp Met Val Glu Gly Asp Lys Tyr Trp	His Ser Ile Ser His	
770	775	780
Leu Gln Pro Glu Thr Ser Tyr Asp Ile Lys	Met Gln Cys Phe Asn	
785	790	795
Glu Gly Glu Ser Glu Phe Ser Asn Val Met	Ile Cys Glu Thr	
800	805	810
Lys Ala Arg Lys Ser Ser Gly Gln Pro Gly	Arg Leu Pro Pro Pro	
815	820	825
Thr Leu Ala Pro Pro Gln Pro Pro Leu Pro	Glu Thr Ile Glu Arg	
830	835	840
Pro Val Gly Thr Gly Ala Met Val Ala Arg	Ser Ser Asp Leu Pro	
845	850	855

Tyr Leu Ile Val Gly Val Val Leu Gly Ser Ile Val Leu Ile Ile
 860 865 870
 Val Thr Phe Ile Pro Phe Cys Leu Trp Arg Ala Trp Ser Lys Gln
 875 880 885
 Lys His Thr Thr Asp Leu Gly Phe Pro Arg Ser Ala Leu Pro Pro
 890 895 900
 Ser Cys Pro Tyr Thr Met Val Pro Leu Gly Gly Leu Pro Gly His
 905 910 915
 Gln Ala Ser Gly Gln Pro Tyr Leu Ser Gly Ile Ser Gly Arg Ala
 920 925 930
 Cys Ala Asn Gly Ile His Met Asn Arg Gly Cys Pro Ser Ala Ala
 935 940 945
 Val Gly Tyr Pro Gly Met Lys Pro Gln Gln His Cys Pro Gly Glu
 950 955 960
 Leu Gln Gln Gln Ser Asp Thr Ser Ser Leu Leu Arg Gln Thr His
 965 970 975
 Leu Gly Asn Gly Tyr Asp Pro Gln Ser His Gln Ile Thr Arg Gly
 980 985 990
 Pro Lys Ser Ser Pro Asp Glu Gly Ser Phe Leu Tyr Thr Leu Pro
 995 1000 1005
 Asp Asp Ser Thr His Gln Leu Leu Gln Pro His His Asp Cys Cys
 1010 1015 1020
 Gln Arg Gln Glu Gln Pro Ala Ala Val Gly Gln Ser Gly Val Arg
 1025 1030 1035
 Arg Ala Pro Asp Ser Pro Val Leu Glu Ala Val Trp Asp Pro Pro
 1040 1045 1050
 Phe His Ser Gly Pro Pro Cys Cys Leu Gly Leu Val Pro Val Glu
 1055 1060 1065
 Glu Val Asp Ser Pro Asp Ser Cys Gln Val Ser Gly Gly Asp Trp
 1070 1075 1080
 Cys Pro Gln His Pro Val Gly Ala Tyr Val Gly Gln Glu Pro Gly
 1085 1090 1095
 Met Gln Leu Ser Pro Gly Pro Leu Val Arg Val Ser Phe Glu Thr
 1100 1105 1110
 Pro Pro Leu Thr Ile
 1115

<210> 59
 <211> 25
 <212> DNA
 <213> Artificial

<220>
<221> Artificial sequence
<222> 1-25
<223> Synthetic construct.

<400> 59
gggaaacaca gcagtcattg cctgc 25

<210> 60
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-24
<223> Synthetic construct.

<400> 60
gcacacgtac cctgtcgctg gagc 24

<210> 61
<211> 42
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-42
<223> Synthetic construct.

<400> 61
caccccaaag cccaggtccg gtacagcgta aaacaagagt gg 42

<210> 62
<211> 1661
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 678
<223> unknown base

<400> 62
cgggaggctg ggtcgcatg atccggaccc cattgtcgcc 50
cgccctgctcc tcccaggctc ccgcggccga ccccccgcga acatgcagcc 100
cacggggccgc gagggttccc gcgcgctcag ccggcggtat ctgcggcg 150
tgctgctcct gctactgctg ctgctgctgc ggcagccgt aacccgcgcg 200
gagaccacgc cgggcggccc cagagccctc tccacgctgg gctccccag 250
cctcttcacc acgcccggtg tccccagcgc cctcaactacc ccaggcctca 300
ctacgccagg caccccaaa accctggacc ttcggggctg cgccgagcc 350

ctgatgcgga gtttccact cgtggacggc cacaatgacc tgccccaggt 400
cctgagacag cgttacaaga atgtgcttca ghatgttaac ctgcgaaatt 450
tcagccatgg tcagaccagc ctggacaggg ttagagacgg cctcgtgggt 500
gcccagttct ggtcagcctc cgtctcatgc cagtcggcagg accagactgc 550
cgtgcgcctc gccctggagc agattgaccc tatttcaccgc atgtgtgcct 600
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agacaccaca tgtacaccaa cgtcagcggga ttgacaagct ttgggtgagaa 850
agtagtagag gagttgaacc gcctggcat gatgatagat ttgtcctatg 900
catcgacac cttgataaga agggtcctgg aagtgtctca ggctcctgtg 950
atcttctccc actcagctgc cagagctgtg tgtgacaatt tggtaatgt 1000
tcccgtatgt atcctgcagc ttctgaagaa cgggtggcatc gtgatggta 1050
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cgggatttgtt gaaaattatg acgggactgg ccgggtccct caggggctgg 1200
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cttcagacaa gtggaaaagg tgagagagga gagcaggcg cagagcccg 1350
tggaggctga gtttccatgg gggcaactga gcacatccctg ccactccac 1400
ctcgtgcctc agaatggaca ccaggctact catctggagg tgaccaagca 1450
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ttccaggcct tgggtgtctt gccaccatcc caacccatcc ccagtggctc 1550
tgctgacaca gtcggtcccc gcagaggtca ctgtggcaaa gcctcacaaa 1600
gccccctctc ctagttcatt cacaaggata tgctgagaat aaacatgtta 1650
cacatggaaa a 1661

<210> 63
<211> 487
<212> PRT
<213> Homo sapiens

<220>
<221> unsure
<222> 196, 386
<223> unknown amino acid

<400> 63

Met	Gln	Pro	Thr	Gly	Arg	Glu	Gly	Ser	Arg	Ala	Leu	Ser	Arg	Arg
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Tyr	Leu	Arg	Arg	Leu	Arg									
	20							25						30
Gln	Pro	Val	Thr	Arg	Ala	Glu	Thr	Thr	Pro	Gly	Ala	Pro	Arg	Ala
		35					40							45
Leu	Ser	Thr	Leu	Gly	Ser	Pro	Ser	Leu	Phe	Thr	Thr	Pro	Gly	Val
			50					55						60
Pro	Ser	Ala	Leu	Thr	Thr	Pro	Gly	Leu	Thr	Thr	Pro	Gly	Thr	Pro
				65				70						75
Lys	Thr	Leu	Asp	Leu	Arg	Gly	Arg	Ala	Gln	Ala	Leu	Met	Arg	Ser
				80				85						90
Phe	Pro	Leu	Val	Asp	Gly	His	Asn	Asp	Leu	Pro	Gln	Val	Leu	Arg
			95					100						105
Gln	Arg	Tyr	Lys	Asn	Val	Leu	Gln	Asp	Val	Asn	Leu	Arg	Asn	Phe
				110					115					120
Ser	His	Gly	Gln	Thr	Ser	Leu	Asp	Arg	Leu	Arg	Asp	Gly	Leu	Val
				125				130						135
Gly	Ala	Gln	Phe	Trp	Ser	Ala	Ser	Val	Ser	Cys	Gln	Ser	Gln	Asp
			140					145						150
Gln	Thr	Ala	Val	Arg	Leu	Ala	Leu	Glu	Gln	Ile	Asp	Leu	Ile	His
			155					160						165
Arg	Met	Cys	Ala	Ser	Tyr	Ser	Glu	Leu	Glu	Leu	Val	Thr	Ser	Ala
			170					175						180
Glu	Gly	Leu	Asn	Ser	Ser	Gln	Lys	Leu	Ala	Cys	Leu	Ile	Gly	Val
			185					190						195
Xaa	Gly	Gly	His	Ser	Leu	Asp	Ser	Ser	Leu	Ser	Val	Leu	Arg	Ser
			200					205						210
Phe	Tyr	Val	Leu	Gly	Val	Arg	Tyr	Leu	Thr	Leu	Thr	Phe	Thr	Cys
			215					220						225
Ser	Thr	Pro	Trp	Ala	Glu	Ser	Ser	Thr	Lys	Phe	Arg	His	His	Met
			230					235						240
Tyr	Thr	Asn	Val	Ser	Gly	Leu	Thr	Ser	Phe	Gly	Glu	Lys	Val	Val
			245					250						255
Glu	Glu	Leu	Asn	Arg	Leu	Gly	Met	Met	Ile	Asp	Leu	Ser	Tyr	Ala

260	265	270
Ser Asp Thr Leu Ile Arg Arg Val Leu Glu Val Ser Gln Ala Pro		
275	280	285
Val Ile Phe Ser His Ser Ala Ala Arg Ala Val Cys Asp Asn Leu		
290	295	300
Leu Asn Val Pro Asp Asp Ile Leu Gln Leu Leu Lys Asn Gly Gly		
305	310	315
Ile Val Met Val Thr Leu Ser Met Gly Val Leu Gln Cys Asn Leu		
320	325	330
Leu Ala Asn Val Ser Thr Val Ala Asp His Phe Asp His Ile Arg		
335	340	345
Ala Val Ile Gly Ser Glu Phe Ile Gly Ile Gly Gly Asn Tyr Asp		
350	355	360
Gly Thr Gly Arg Phe Pro Gln Gly Leu Glu Asp Val Ser Thr Tyr		
365	370	375
Pro Val Leu Ile Glu Glu Leu Leu Ser Arg Xaa Trp Ser Glu Glu		
380	385	390
Glu Leu Gln Gly Val Leu Arg Gly Asn Leu Leu Arg Val Phe Arg		
395	400	405
Gln Val Glu Lys Val Arg Glu Glu Ser Arg Ala Gln Ser Pro Val		
410	415	420
Glu Ala Glu Phe Pro Tyr Gly Gln Leu Ser Thr Ser Cys His Ser		
425	430	435
His Leu Val Pro Gln Asn Gly His Gln Ala Thr His Leu Glu Val		
440	445	450
Thr Lys Gln Pro Thr Asn Arg Val Pro Trp Arg Ser Ser Asn Ala		
455	460	465
Ser Pro Tyr Leu Val Pro Gly Leu Val Ala Ala Ala Thr Ile Pro		
470	475	480
Thr Phe Thr Gln Trp Leu Cys		
485		

<210> 64
 <211> 25
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-25
 <223> Synthetic construct.

<400> 64

ccttcacccg cagtacacca tggc 25
<210> 65
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-25
<223> Synthetic construct.

<400> 65
gtcacacaca gctctggcag ctgag 25

<210> 66
<211> 47
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-47
<223> Synthetic construct.

<400> 66
ccaagttcag acaccacatg tacaccaacg tcagcggatt gacaagc 47

<210> 67
<211> 1564
<212> DNA
<213> Homo sapiens

<400> 67
tgctaggctc tgtcccacaa tgcacccgag agcaggagct gaaagcctct 50
aacacccaca gatccctcta tgactgcaat gtgaggtgtc cggctttgct 100
ggcccagcaa gcctgataag catgaagctc ttatctttgg tggctgtggt 150
cgggtgtttg ctggtgcccc cagctgaagc caacaagagt tctgaagata 200
tccggtgcaa atgcatctgt ccaccttata gaaacatcag tggcacatt 250
tacaaccaga atgtatccca gaaggactgc aactgcctgc acgtggtgga 300
gccccatgcca gtgcctggcc atgacgtgga ggcctactgc ctgctgtgcg 350
agtgcaggtt cggaggcgcc agcaccacca ccatcaaggt catcattgtc 400
atctacactgt ccgtgggtgg tgcctgttg ctctacatgg ctttcctgtat 450
gctgggtggac cctctgatcc gaaagccgga tgcatacact gagcaactgc 500
acaatgagga ggagaatgag gatgctcgct ctatggcagc agctgctgca 550
tccctcgggg gaccccgagc aaacacagtc ctggagcgtg tggaaagggtgc 600

ccagcagcgg tggaagctgc aggtgcagga gcagcggaaag acagtctcg 650
atcggcacaa gatgctcagc tagatggct ggtgtggttg ggtcaaggcc 700
ccaacaccat ggctgccagc ttccaggctg gacaaagcag ggggctactt 750
ctcccttccc tcgggtccag tcttccctt aaaagcctgt ggcattttc 800
ctccttctcc ctaactttag aaatgttga cttggctatt ttgattaggg 850
aagagggatg tggctctga tctctgttgc cttctgggt ctttggggtt 900
gaagggaggg ggaaggcagg ccagaaggaa atggagacat tcgaggcggc 950
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gttcctttct gcagtgggtc ttatcaccac ctccctccca gccccggcgc 1150
ctcagccccca gccccagctc cagccctgag gacagctctg atgggagagc 1200
tgggccccct gagcccactg ggtttcagg gtgcactgga agctgggtt 1250
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ctctgctgcc ggtcccctca cctgcacttg aggggtctgg gcagtccctc 1350
ctctccccag tgtccacagt cactgagcca gacggtcggt tggAACatga 1400
gactcgaggc tgagcgtgga tctgaacacc acagccctg tacttgggtt 1450
gcctcttgtc cctgaacttc gttgtaccag tgcatggaga gaaaattttg 1500
tcctcttgtc ttagagttgt gtgtaaatca aggaagccat cattaaattt 1550
ttttatttct ctca 1564

<210> 68
<211> 183
<212> PRT
<213> Homo sapiens

<400> 68
Met Lys Leu Leu Ser Leu Val Ala Val Val Gly Cys Leu Leu Val
1 5 10 15
Pro Pro Ala Glu Ala Asn Lys Ser Ser Glu Asp Ile Arg Cys Lys
20 25 30
Cys Ile Cys Pro Pro Tyr Arg Asn Ile Ser Gly His Ile Tyr Asn
35 40 45
Gln Asn Val Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu
50 55 60

Pro	Met	Pro	Val	Pro	Gly	His	Asp	Val	Glu	Ala	Tyr	Cys	Leu	Leu
														75
Cys	Glu	Cys	Arg	Tyr	Glu	Glu	Arg	Ser	Thr	Thr	Thr	Ile	Lys	Val
														90
Ile	Ile	Val	Ile	Tyr	Leu	Ser	Val	Val	Gly	Ala	Leu	Leu	Leu	Tyr
														105
Met	Ala	Phe	Leu	Met	Leu	Val	Asp	Pro	Leu	Ile	Arg	Lys	Pro	Asp
														120
Ala	Tyr	Thr	Glu	Gln	Leu	His	Asn	Glu	Glu	Glu	Asn	Glu	Asp	Ala
														135
Arg	Ser	Met	Ala	Ala	Ala	Ala	Ser	Leu	Gly	Gly	Pro	Arg	Ala	
														150
Asn	Thr	Val	Leu	Glu	Arg	Val	Glu	Gly	Ala	Gln	Gln	Arg	Trp	Lys
														165
Leu	Gln	Val	Gln	Glu	Gln	Arg	Lys	Thr	Val	Phe	Asp	Arg	His	Lys
														180
Met	Leu	Ser												

<210> 69
 <211> 3170
 <212> DNA
 <213> Homo sapiens

<400> 69
 agcgggtctc gcttgggttc cgctaatttc tgtcctgagg cgtgagactg 50
 agttcatagg gtcctgggtc cccgaaccag gaagggttga gggAACACAA 100
 tctgcaagcc cccgcgaccc aagtgagggg ccccggttgc gggcctcc 150
 tccctttgca ttccccacccc tccgggcttt gcgtttcct ggggacccccc 200
 tcgcccggag atggccgcgt tgatgcggag caaggattcg tcctgctgcc 250
 tgctcctact ggccgcgtg ctgatggtgg agagctcaca gatcggcagt 300
 tcgcgggcca aactcaactc catcaagtcc tctctggcg gggagacgcc 350
 tggtcaggcc gccaatcgat ctgcggcat gtaccaagga ctggcattcg 400
 gcggcagtaa gaaggcAAA aacctggggc aggctaccc ttgttagcagt 450
 gataaggagt gtgaagttgg gaggtattgc cacagtcccc accaaggatc 500
 atcggcctgc atgggtgtc ggagaaaaaa gaagcgctgc caccgagatg 550
 gcatgtgctg ccccagtacc cgctgcaata atggcatctg tatcccagtt 600
 actgaaagca tcttaacccc tcacatcccg gctctggatg gtactcggca 650

cagagatcga aaccacggc attactcaaa ccatgacttg ggatggcaga 700
atcttaggaag accacacact aagatgtcac atataaaagg gcatgaagga 750
gaccctgcc tacgatcatc agactgcatt gaagggttt gctgtgctcg 800
tcatttctgg accaaaatct gcaaaccagt gctccatcag ggggaagtct 850
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tgcgactgtg cgaaggcct gtctgcaaa gtatggaaag atgccaccta 950
ctcctccaaa gccagactcc atgtgtgtca gaaaatttga tcaccattga 1000
ggaacatcat caattgcaga ctgtgaagtt gtgtatttaa tgcattatag 1050
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gtgataagaa tatagatgtat cacaaggaa gagaaagaaa acatgaactg 1150
aatagattag aatgggtgac aaatgcagtg cagccagtgt ttccattatg 1200
caacttgtct atgtaaataa tgtacacatt tgtggaaat gctattatta 1250
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ttatacaaat aacctacatg ccagattctt attcaacgtt agagtttaac 1400
aaaatactcc tagaataact tgttatacaa taggttctaa aaataaaatt 1450
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ttcacagatg gcaaaaaat ttaaagatgt ccaatatacg tggaaaaga 1900
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aaatataagt aggataactt gtaaaacctg catattgcta atctatagac 2500
accacagttt cttaattctt tgaaaccact ttactacttt ttttaaactt 2550
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tctttactt aaatccatc tgcagtctca aatttaagtt ctcccagtag 2700
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tatttactaa gatgattaag acttacattt tctgcacagg tctgcaaaaa 2800
caaaaattat aaactagtcc atccaagaac caaagttgt ataaacaggt 2850
tgctataagc ttgtgaaatg aaaatggaac atttcaatca aacatttcct 2900
atataacaat tattatattt acaatttggt ttctgcaata ttttcttat 2950
gtccaccctt ttaaaaatta ttatggaaag taatttattt acagggaaatg 3000
ttaatgagat gtatttctt atagagatat ttcttacaga aagctttgta 3050
gcagaatata tttgcagcta ttgactttgt aatttaggaa aatgtataa 3100
taagataaaa tctattaaat tttctccctc taaaaactga aaaaaaaaaa 3150
aaaaaaaaaaa aaaaaaaaaa 3170

<210> 70
<211> 259
<212> PRT
<213> Homo sapiens

<400> 70
Met Ala Ala Leu Met Arg Ser Lys Asp Ser Ser Cys Cys Leu Leu
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Leu Leu Ala Ala Val Leu Met Val Glu Ser Ser Gln Ile Gly Ser
20 25 30
Ser Arg Ala Lys Leu Asn Ser Ile Lys Ser Ser Leu Gly Gly Glu
35 40 45

Thr Pro Gly Gln Ala Ala Asn Arg Ser Ala Gly Met Tyr Gln Gly
 50 55 60
 Leu Ala Phe Gly Gly Ser Lys Lys Gly Lys Asn Leu Gly Gln Ala
 65 70 75
 Tyr Pro Cys Ser Ser Asp Lys Glu Cys Glu Val Gly Arg Tyr Cys
 80 85 90
 His Ser Pro His Gln Gly Ser Ser Ala Cys Met Val Cys Arg Arg
 95 100 105
 Lys Lys Lys Arg Cys His Arg Asp Gly Met Cys Cys Pro Ser Thr
 110 115 120
 Arg Cys Asn Asn Gly Ile Cys Ile Pro Val Thr Glu Ser Ile Leu
 125 130 135
 Thr Pro His Ile Pro Ala Leu Asp Gly Thr Arg His Arg Asp Arg
 140 145 150
 Asn His Gly His Tyr Ser Asn His Asp Leu Gly Trp Gln Asn Leu
 155 160 165
 Gly Arg Pro His Thr Lys Met Ser His Ile Lys Gly His Glu Gly
 170 175 180
 Asp Pro Cys Leu Arg Ser Ser Asp Cys Ile Glu Gly Phe Cys Cys
 185 190 195
 Ala Arg His Phe Trp Thr Lys Ile Cys Lys Pro Val Leu His Gln
 200 205 210
 Gly Glu Val Cys Thr Lys Gln Arg Lys Lys Gly Ser His Gly Leu
 215 220 225
 Glu Ile Phe Gln Arg Cys Asp Cys Ala Lys Gly Leu Ser Cys Lys
 230 235 240
 Val Trp Lys Asp Ala Thr Tyr Ser Ser Lys Ala Arg Leu His Val
 245 250 255
 Cys Gln Lys Ile

<210> 71
 <211> 1809
 <212> DNA
 <213> Homo sapiens

<400> 71
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 tggcctccca aagtgttggg attacaggcg tgagccaccg cgcccgcca 100
 acatcacgtt tttaaaaatt gatttcttca aattcatggc aaatatttcc 150
 cttcccttta acttctttag tcagaatgag gaaggatagc tgcatttt 200

tagtcagtt tcattgcata gtaatattt catgtat 250
atatttagt aattcatatg ttttagatta tagtttaa catacttg 300
aaaatactg atgtttta aagccttggg cagaattct gtattgtga 350
ggatttgttc ttttatcccc cttaaagt catccgtcct tggctcagga 400
tttggagagc ttgcaccacc aaaaatggca aacatcacca gctccca 450
tttggaccag ttgaaagctc cgagtttggg ccagttacc accacccaa 500
gtacacagca gaatagtaca agtcacccta caactactac ttcttggac 550
ctcaagcccc caacatccca gtcctcagtc ctcagtcac ttgacttcaa 600
atctcaacct gagccatccc cagttcttag ccagttgagc cagcgacaac 650
agcaccagag ccaggcagtc actgttcctc ctcctggttt ggagtccttt 700
ccttcccagg caaaacttcg agaatcaaca cctggagaca gtccctccac 750
tgtgaacaag ctttgcagc ttcccagcac gaccattgaa aatatctctg 800
tgtctgtcca ccagccacag cccaaacaca tcaaacttgc taagcggcgg 850
ataccccaag cttctaagat cccagcttct gcagtggaaa tgcctggttc 900
agcagatgtc acaggattaa atgtgcagtt tgggctctg gaatttgggt 950
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cccataccaa agccctgtga gttcatcaga gtcagctcca ggaaccatca 1250
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accctggca acatggtaa actctgttc tactaaaata cgaaaaacta 1700
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ctgaaaaga 1809

<210> 72
<211> 363
<212> PRT
<213> Homo sapiens

<400> 72

Met	Cys	Phe	Lys	Ala	Leu	Gly	Arg	Asn	Ser	Val	Leu	Leu	Arg	Ile
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Cys	Ser	Phe	Ile	Pro	Leu	Leu	Lys	Ser	Ser	Val	Leu	Gly	Ser	Gly
					20					25				30
Phe	Gly	Glu	Leu	Ala	Pro	Pro	Lys	Met	Ala	Asn	Ile	Thr	Ser	Ser
					35					40				45
Gln	Ile	Leu	Asp	Gln	Leu	Lys	Ala	Pro	Ser	Leu	Gly	Gln	Phe	Thr
					50					55				60
Thr	Thr	Pro	Ser	Thr	Gln	Gln	Asn	Ser	Thr	Ser	His	Pro	Thr	Thr
					65					70				75
Thr	Thr	Ser	Trp	Asp	Leu	Lys	Pro	Pro	Thr	Ser	Gln	Ser	Ser	Val
					80					85				90
Leu	Ser	His	Leu	Asp	Phe	Lys	Ser	Gln	Pro	Glu	Pro	Ser	Pro	Val
					95					100				105
Leu	Ser	Gln	Leu	Ser	Gln	Arg	Gln	Gln	His	Gln	Ser	Gln	Ala	Val
					110					115				120
Thr	Val	Pro	Pro	Pro	Gly	Leu	Glu	Ser	Phe	Pro	Ser	Gln	Ala	Lys
					125					130				135
Leu	Arg	Glu	Ser	Thr	Pro	Gly	Asp	Ser	Pro	Ser	Thr	Val	Asn	Lys
					140					145				150
Leu	Leu	Gln	Leu	Pro	Ser	Thr	Thr	Ile	Glu	Asn	Ile	Ser	Val	Ser
					155					160				165
Val	His	Gln	Pro	Gln	Pro	Lys	His	Ile	Lys	Leu	Ala	Lys	Arg	Arg
					170					175				180
Ile	Pro	Pro	Ala	Ser	Lys	Ile	Pro	Ala	Ser	Ala	Val	Glu	Met	Pro
					185					190				195
Gly	Ser	Ala	Asp	Val	Thr	Gly	Leu	Asn	Val	Gln	Phe	Gly	Ala	Leu
					200					205				210
Glu	Phe	Gly	Ser	Glu	Pro	Ser	Leu	Ser	Glu	Phe	Gly	Ser	Ala	Pro
					215					220				225

Ser Ser Glu Asn Ser Asn Gln Ile Pro Ile Ser Leu Tyr Ser Lys
230 235 240
Ser Leu Ser Glu Pro Leu Asn Thr Ser Leu Ser Met Thr Ser Ala
245 250 255
Val Gln Asn Ser Thr Tyr Thr Ser Val Ile Thr Ser Cys Ser
260 265 270
Leu Thr Ser Ser Ser Leu Asn Ser Ala Ser Pro Val Ala Met Ser
275 280 285
Ser Ser Tyr Asp Gln Ser Ser Val His Asn Arg Ile Pro Tyr Gln
290 295 300
Ser Pro Val Ser Ser Ser Glu Ser Ala Pro Gly Thr Ile Met Asn
305 310 315
Gly His Gly Gly Gly Arg Ser Gln Gln Thr Leu Asp Ser Lys Tyr
320 325 330
Ser Ser Lys Leu Leu Ser Trp Leu Val Pro Thr Lys Gln Arg
335 340 345
Lys Arg Ile Ala His Val Met Trp Lys Thr Pro Val Gly Gln Trp
350 355 360
Leu Ile Arg

<210> 73
<211> 26
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-26
<223> Synthetic construct.

<400> 73
aattcatggc aaatatttcc cttccc 26

<210> 74
<211> 22
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-22
<223> Synthetic construct.

<400> 74
tggtaaactg gcccaaactc gg 22

<210> 75
<211> 50

<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-50
<223> Synthetic construct

<400> 75
ttaaaagtcat ccgtccttgg ctcaggattt ggagagctt caccaccaaa 50

<210> 76
<211> 1989
<212> DNA
<213> Homo sapiens

<400> 76
ggcgagtgg acaaaggctg gggctggcg gggccatgg cgctgccatc 50
ccgaatcctg ctttgaaac ttgtgcttct gcagagctct gctgttctcc 100
tgcactcagc ggtggaggag acggacgcgg ggctgtacac ctgcaacctg 150
caccatcact actgccaccc ctacgagagc ctggccgtcc gcctggaggt 200
caccgacggc ccccccggcca ccccccgccta ctgggacggc gagaaggagg 250
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gggcacgtgt ggaccgaccg gcacgtggag gaggctcaac aggtggtgca 350
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aactgcaaat agggaggccc tgggctcctg gctgggccag cagctgcacc 1100
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ccactctcag caccacat ttgcattgc ttgtggaccc gccaccatca 1950
caataaagtc cccatctgat tttaaaaaaa aaaaaaaaaa 1989

<210> 77

<211> 341

<212> PRT

<213> Homo sapiens

<400> 77

Met	Ala	Leu	Pro	Ser	Arg	Ile	Leu	Leu	Trp	Lys	Leu	Val	Leu	Leu
1									10					15

Gln	Ser	Ser	Ala	Val	Leu	Leu	His	Ser	Ala	Val	Glu	Glu	Thr	Asp
											25			30

Ala	Gly	Leu	Tyr	Thr	Cys	Asn	Leu	His	His	His	Tyr	Cys	His	Leu
											35		40	45

Tyr	Glu	Ser	Leu	Ala	Val	Arg	Leu	Glu	Val	Thr	Asp	Gly	Pro	Pro
										50		55		60

Ala	Thr	Pro	Ala	Tyr	Trp	Asp	Gly	Glu	Lys	Glu	Val	Leu	Ala	Val
									65		70		75	

Ala Arg Gly Ala Pro Ala Leu Leu Thr Cys Val Asn Arg Gly His
 80 85 90

Val Trp Thr Asp Arg His Val Glu Glu Ala Gln Gln Val Val His
 95 100 105

Trp Asp Arg Gln Pro Pro Gly Val Pro His Asp Arg Ala Asp Arg
 110 115 120

Leu Leu Asp Leu Tyr Ala Ser Gly Glu Arg Arg Ala Tyr Gly Pro
 125 130 135

Leu Phe Leu Arg Asp Arg Val Ala Val Gly Ala Asp Ala Phe Glu
 140 145 150

Arg Gly Asp Phe Ser Leu Arg Ile Glu Pro Leu Glu Val Ala Asp
 155 160 165

Glu Gly Thr Tyr Ser Cys His Leu His His His Tyr Cys Gly Leu
 170 175 180

His Glu Arg Arg Val Phe His Leu Thr Val Ala Glu Pro His Ala
 185 190 195

Glu Pro Pro Pro Arg Gly Ser Pro Gly Asn Gly Ser Ser His Ser
 200 205 210

Gly Ala Pro Gly Pro Asp Pro Thr Leu Ala Arg Gly His Asn Val
 215 220 225

Ile Asn Val Ile Val Pro Glu Ser Arg Ala His Phe Phe Gln Gln
 230 235 240

Leu Gly Tyr Val Leu Ala Thr Leu Leu Leu Phe Ile Leu Leu Leu
 245 250 255

Val Thr Val Leu Leu Ala Ala Arg Arg Arg Arg Gly Gly Tyr Glu
 260 265 270

Tyr Ser Asp Gln Lys Ser Gly Lys Ser Lys Gly Lys Asp Val Asn
 275 280 285

Leu Ala Glu Phe Ala Val Ala Ala Gly Asp Gln Met Leu Tyr Arg
 290 295 300

Ser Glu Asp Ile Gln Leu Asp Tyr Lys Asn Asn Ile Leu Lys Glu
 305 310 315

Arg Ala Glu Leu Ala His Ser Pro Leu Pro Ala Lys Tyr Ile Asp
 320 325 330

Leu Asp Lys Gly Phe Arg Lys Glu Asn Cys Lys
 335 340

<210> 78
 <211> 2243
 <212> DNA
 <213> Homo sapiens

<400> 78
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cgccccctgg cctgcagagg cccgaggacc gcttctgtgg cacatacata 200
atcttcttca gcctggcat tggcagtcta ctggcatgga acttctttat 250
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gccattgggtt caagggcgta ataaatactt gcgtattcaa aaa 2243

<210> 79

<211> 475

<212> PRT

<213> Homo sapiens

<400> 79

Met Ala Val Val Ser Glu Asp Asp Phe Gln His Ser Ser Asn Ser
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Thr Tyr Gly Thr Thr Ser Ser Ser Leu Arg Ala Asp Gln Glu Ala
20 25 30

Leu Leu Glu Lys Leu Leu Asp Arg Pro Pro Pro Gly Leu Gln Arg
35 40 45

Pro Glu Asp Arg Phe Cys Gly Thr Tyr Ile Ile Phe Phe Ser Leu
50 55 60

Gly Ile Gly Ser Leu Leu Pro Trp Asn Phe Phe Ile Thr Ala Lys
65 70 75

Glu Tyr Trp Met Phe Lys Leu Arg Asn Ser Ser Ser Pro Ala Thr
80 85 90

Gly Glu Asp Pro Glu Gly Ser Asp Ile Leu Asn Tyr Phe Glu Ser
95 100 105

Tyr Leu Ala Val Ala Ser Thr Val Pro Ser Met Leu Cys Leu Val
 110 115 120
 Ala Asn Phe Leu Leu Val Asn Arg Val Ala Val His Ile Arg Val
 125 130 135
 Leu Ala Ser Leu Thr Val Ile Leu Ala Ile Phe Met Val Ile Thr
 140 145 150
 Ala Leu Val Lys Val Asp Thr Ser Ser Trp Thr Arg Gly Phe Phe
 155 160 165
 Ala Val Thr Ile Val Cys Met Val Ile Leu Ser Gly Ala Ser Thr
 170 175 180
 Val Phe Ser Ser Ser Ile Tyr Gly Met Thr Gly Ser Phe Pro Met
 185 190 195
 Arg Asn Ser Gln Ala Leu Ile Ser Gly Gly Ala Met Gly Gly Thr
 200 205 210
 Val Ser Ala Val Ala Ser Leu Val Asp Leu Ala Ala Ser Ser Asp
 215 220 225
 Val Arg Asn Ser Ala Leu Ala Phe Phe Leu Thr Ala Thr Ile Phe
 230 235 240
 Leu Val Leu Cys Met Gly Leu Tyr Leu Leu Leu Ser Arg Leu Glu
 245 250 255
 Tyr Ala Arg Tyr Tyr Met Arg Pro Val Leu Ala Ala His Val Phe
 260 265 270
 Ser Gly Glu Glu Glu Leu Pro Gln Asp Ser Leu Ser Ala Pro Ser
 275 280 285
 Val Ala Ser Arg Phe Ile Asp Ser His Thr Pro Pro Leu Arg Pro
 290 295 300
 Ile Leu Lys Lys Thr Ala Ser Leu Gly Phe Cys Val Thr Tyr Val
 305 310 .. 315
 Phe Phe Ile Thr Ser Leu Ile Tyr Pro Ala Val Cys Thr Asn Ile
 320 325 330
 Glu Ser Leu Asn Lys Gly Ser Gly Ser Leu Trp Thr Thr Lys Phe
 335 340 345
 Phe Ile Pro Leu Thr Thr Phe Leu Leu Tyr Asn Phe Ala Asp Leu
 350 355 360
 Cys Gly Arg Gln Leu Thr Ala Trp Ile Gln Val Pro Gly Pro Asn
 365 370 375
 Ser Lys Ala Leu Pro Gly Phe Val Leu Leu Arg Thr Cys Leu Ile
 380 385 390
 Pro Leu Phe Val Leu Cys Asn Tyr Gln Pro Arg Val His Leu Lys

395	400	405
Thr Val Val Phe Gln Ser Asp Val Tyr Pro Ala Leu Leu Ser Ser		
410	415	420
Leu Leu Gly Leu Ser Asn Gly Tyr Leu Ser Thr Leu Ala Leu Leu		
425	430	435
Tyr Gly Pro Lys Ile Val Pro Arg Glu Leu Ala Glu Ala Thr Gly		
440	445	450
Val Val Met Ser Phe Tyr Val Cys Leu Gly Leu Thr Leu Gly Ser		
455	460	465
Ala Cys Ser Thr Leu Leu Val His Leu Ile		
470	475	

<210> 80
<211> 22
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-22
<223> Synthetic construct.

<400> 80
ttttgcggtc accattgtct gc 22

<210> 81
<211> 23
<212> DNA
<213> Homo sapiens

<220>
<221> Artificial sequence
<222> 1-23
<223> Synthetic construct.

<400> 81
cgttaggtgac acagaagccc agg 23

<210> 82
<211> 49
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-49
<223> Synthetic construct.

<400> 82
tacggcatga ccggctcctt tcctatgagg aactccagg cactgatat 49

<210> 83
<211> 1844

<212> DNA
<213> Homo sapiens

<400> 83
gacagtggag ggcagtggag aggaccgcgc tgtcctgctg tcaccaagag 50
ctggagacac catctccac cgagagtcat ggccccattg gccctgcacc 100
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aaggctgaac gcagccaaga ccccttcgag aaatgcatgc aggatcctga 200
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aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1844

<210> 84
<211> 567
<212> PRT
<213> Homo sapiens

<400> 84

Met	Ala	Pro	Leu	Ala	Leu	His	Leu	Leu	Val	Leu	Val	Pro	Ile	Leu	
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Leu	Ser	Leu	Val	Ala	Ser	Gln	Asp	Trp	Lys	Ala	Glu	Arg	Ser	Gln	
															30
Asp	Pro	Phe	Glu	Lys	Cys	Met	Gln	Asp	Pro	Asp	Tyr	Glu	Gln	Leu	
															45
Leu	Lys	Val	Val	Thr	Trp	Gly	Leu	Asn	Arg	Thr	Leu	Lys	Pro	Gln	
															60
Arg	Val	Ile	Val	Val	Gly	Ala	Gly	Val	Ala	Gly	Leu	Val	Ala	Ala	
															75
Lys	Val	Leu	Ser	Asp	Ala	Gly	His	Lys	Val	Thr	Ile	Leu	Glu	Ala	
															90
Asp	Asn	Arg	Ile	Gly	Gly	Arg	Ile	Phe	Thr	Tyr	Arg	Asp	Gln	Asn	
															105
Thr	Gly	Trp	Ile	Gly	Glu	Leu	Gly	Ala	Met	Arg	Met	Pro	Ser	Ser	
															120
His	Arg	Ile	Leu	His	Lys	Leu	Cys	Gln	Gly	Leu	Gly	Leu	Asn	Leu	
															135
Thr	Lys	Phe	Thr	Gln	Tyr	Asp	Lys	Asn	Thr	Trp	Thr	Glu	Val	His	
															150
Glu	Val	Lys	Leu	Arg	Asn	Tyr	Val	Val	Glu	Lys	Val	Pro	Glu	Lys	
															165
155									160						

Leu Gly Tyr Ala Leu Arg Pro Gln Glu Lys Gly His Ser Pro Glu
 170 175 180
 Asp Ile Tyr Gln Met Ala Leu Asn Gln Ala Leu Lys Asp Leu Lys
 185 190 195
 Ala Leu Gly Cys Arg Lys Ala Met Lys Lys Phe Glu Arg His Thr
 200 205 210
 Leu Leu Glu Tyr Leu Leu Gly Glu Gly Asn Leu Ser Arg Pro Ala
 215 220 225
 Val Gln Leu Leu Gly Asp Val Met Ser Glu Asp Gly Phe Phe Tyr
 230 235 240
 Leu Ser Phe Ala Glu Ala Leu Arg Ala His Ser Cys Leu Ser Asp
 245 250 255
 Arg Leu Gln Tyr Ser Arg Ile Val Gly Gly Trp Asp Leu Leu Pro
 260 265 270
 Arg Ala Leu Leu Ser Ser Leu Ser Gly Leu Val Leu Leu Asn Ala
 275 280 285
 Pro Val Val Ala Met Thr Gln Gly Pro His Asp Val His Val Gln
 290 295 300
 Ile Glu Thr Ser Pro Pro Ala Arg Asn Leu Lys Val Leu Lys Ala
 305 310 315
 Asp Val Val Leu Leu Thr Ala Ser Gly Pro Ala Val Lys Arg Ile
 320 325 330
 Thr Phe Ser Pro Pro Leu Pro Arg His Met Gln Glu Ala Leu Arg
 335 340 345
 Arg Leu His Tyr Val Pro Ala Thr Lys Val Phe Leu Ser Phe Arg
 350 355 360
 Arg Pro Phe Trp Arg Glu Glu His Ile Glu Gly Gly His Ser Asn
 365 370 375
 Thr Asp Arg Pro Ser Arg Met Ile Phe Tyr Pro Pro Pro Arg Glu
 380 385 390
 Gly Ala Leu Leu Leu Ala Ser Tyr Thr Trp Ser Asp Ala Ala Ala
 395 400 405
 Ala Phe Ala Gly Leu Ser Arg Glu Glu Ala Leu Arg Leu Ala Leu
 410 415 420
 Asp Asp Val Ala Ala Leu His Gly Pro Val Val Arg Gln Leu Trp
 425 430 435
 Asp Gly Thr Gly Val Val Lys Arg Trp Ala Glu Asp Gln His Ser
 440 445 450
 Gln Gly Gly Phe Val Val Gln Pro Pro Ala Leu Trp Gln Thr Glu

455	460	465
Lys Asp Asp Trp Thr Val Pro Tyr Gly Arg Ile Tyr Phe Ala Gly		
470	475	480
Glu His Thr Ala Tyr Pro His Gly Trp Val Glu Thr Ala Val Lys		
485	490	495
Ser Ala Leu Arg Ala Ala Ile Lys Ile Asn Ser Arg Lys Gly Pro		
500	505	510
Ala Ser Asp Thr Ala Ser Pro Glu Gly His Ala Ser Asp Met Glu		
515	520	525
Gly Gln Gly His Val His Gly Val Ala Ser Ser Pro Ser His Asp		
530	535	540
Leu Ala Lys Glu Glu Gly Ser His Pro Pro Val Gln Gly Gln Leu		
545	550	555
Ser Leu Gln Asn Thr Thr His Thr Arg Thr Ser His		
560	565	

<210> 85
 <211> 3316
 <212> DNA
 <213> Homo sapiens

<400> 85
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 ctctggccg gccttctgcc tgcatggacg ctctgaagcc accctgtctc 100
 tggaggaacc acgagcgagg gaagaaggac agggactcgt gtggcaggaa 150
 gaactcagag ccggaaagcc cccattcact agaagcactg agagatgcgg 200
 cccctcgca gggctgaat ttctgtgc tgttcacaaa gatgctttt 250
 atctttaact tttgttttc cccacttccg accccggcgt tgatctgcat 300
 cctgacattt ggagctgcca tttcttgac gctgatcacc agacctaacc 350
 ccgtcttacc tcttcttgac ctgaacaatc agtctgtggg aattgaggaa 400
 ggagcacgga agggggtttc ccagaagaac aatgacctaa caagttgtc 450
 cttctcagat gccaagacta tgtatgaggt ttccaaaga ggactcgctg 500
 tgtctgacaa tggccctgc ttggatata gaaaacaaa ccagccctac 550
 agatggctat cttacaaaca ggtgtctgat agagcagagt acctgggttc 600
 ctgtctcttgcataaaaggaa ataaatcatc accagaccag tttgtcggca 650
 tctttgtca gaataggcca gagtggatca tctccaaatt ggcttggttac 700
 acgtactcta tggtagctgt acctctgtat gacacccctgg gaccagaagc 750

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caccccaaaa ggcattggtg ctgatagggaa atgtagagaa aggcttcacc 850
ccgagcctga aggtgatcat ccttatggac ccctttgatg atgacctgaa 900
gcaaagaggg gagaagagtg gaattgagat cttatcccta tatgatgctg 950
agaacctagg caaagagcac ttcagaaaac ctgtgcctcc tagcccagaa 1000
gacctgagcg tcatctgctt caccagtggg accacaggtg accccaaagg 1050
agccatgata acccatcaaa atattgttc aaatgctgct gccttcctca 1100
aatgtgtgga gcatgcttat gagcccactc ctgatgatgt ggccatatcc 1150
taccccttc tggctcatat gtttgagagg attgtacagg ctgttgta 1200
cagctgtgga gccagagttg gattcttcca agggatatt cggttgctgg 1250
ctgacgacat gaagactttg aagcccacat tgttccgc ggtgcctcga 1300
ctccttaaca ggatctacga taaggtacaa aatgaggcca agacaccctt 1350
gaagaagttc ttgttgaagc tggctgttc cagtaaattc aaagagcttc 1400
aaaagggtat catcaggcat gatagttct gggacaagct catcttgca 1450
aagatccagg acagcctggg cggaaagggtt cgtgtattt tcactggagc 1500
tgccccatg tccacttcag tcatgacatt cttccggca gcaatggat 1550
gtcaggtgta tgaagcttat ggtcaaacag aatgcacagg tggctgtaca 1600
tttacattac ctggggactg gacatcaggt cacgttgggg tgccctggc 1650
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tgaataatga aggagaggc tgcataagg gtacaaacgt gttcaaagga 1750
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gcttcacaca ggagacattt gtcgctggct cccgaatggaa actctgaaga 1850
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gcaccagaga agatagaaaa tatctacaac aggagtcaac cagtgttaca 1950
aattttgtt cacggggaga gcttacggc atccttagta ggagtgggtgg 2000
ttcctgacac agatgtactt ccctcattt cagccaaagct tgggtgaag 2050
ggctcctttg aggaactgtg ccaaaaccaa gttgtaaagg aagccatttt 2100
agaagacttg cagaaaattt gaaagaaag tggcctaaa actttgaac 2150
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ctcttgacac caacattgaa agcaaagcga ggagagctt ccaaatactt 2250
tcggacccaa attgacagcc tgtatgagca catccaggat taggataagg 2300
tacttaagta cctgccggcc cactgtcac tgcttgtgag aaaatggatt 2350
aaaaacttattt cttacatttgc ttgtgcctt ctccttattt ttttttaacc 2400
tgtaaactc taaagccata gctttgtt tatattgaga catataatgt 2450
gtaaaacttag ttcccaaata aatcaatcct gtcttccta tcttcgatgt 2500
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ctatcactca tgtcaatcat atctatgaga caaatgtctc cgatgcttt 2850
ctgcgtaaat taaattgtgt actgaaggaa aaagttttagt cataccaaac 2900
atttcctaaa ctctctagtt agatatctga cttgggagta ttaaaaattt 2950
ggtctatgac atactgtcca aaaggaatgc tgttctaaa gcattattta 3000
cagtaggaac tggggagtaa atctgttccc tacagtttgc tgctgagctg 3050
gaagctgtgg gggaggagt tgacaggtgg gcccagtgaa cttttccagt 3100
aaatgaagca agcactgaat aaaaacctcc tgaactggaa acaaagatct 3150
acaggcaagc aagatgcccac cacaacaggc ttatctctg tgaaggaacc 3200
aactgatctc ccccacccctt ggatttagagt tcctgctcta ctttaccac 3250
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tattacagat aaaaaaa 3316

<210> 86
<211> 739
<212> PRT
<213> Homo sapiens

<400> 86
Met Asp Ala Leu Lys Pro Pro Cys Leu Trp Arg Asn His Glu Arg
1 5 10 15
Gly Lys Lys Asp Arg Asp Ser Cys Gly Arg Lys Asn Ser Glu Pro
20 25 30

Gly Ser Pro His Ser Leu Glu Ala Leu Arg Asp Ala Ala Pro Ser
 35 40 45
 Gln Gly Leu Asn Phe Leu Leu Leu Phe Thr Lys Met Leu Phe Ile
 50 55 60
 Phe Asn Phe Leu Phe Ser Pro Leu Pro Thr Pro Ala Leu Ile Cys
 65 70 75
 Ile Leu Thr Phe Gly Ala Ala Ile Phe Leu Trp Leu Ile Thr Arg
 80 85 90
 Pro Gln Pro Val Leu Pro Leu Leu Asp Leu Asn Asn Gln Ser Val
 95 100 105
 Gly Ile Glu Gly Gly Ala Arg Lys Gly Val Ser Gln Lys Asn Asn
 110 115 120
 Asp Leu Thr Ser Cys Cys Phe Ser Asp Ala Lys Thr Met Tyr Glu
 125 130 135
 Val Phe Gln Arg Gly Leu Ala Val Ser Asp Asn Gly Pro Cys Leu
 140 145 150
 Gly Tyr Arg Lys Pro Asn Gln Pro Tyr Arg Trp Leu Ser Tyr Lys
 155 160 165
 Gln Val Ser Asp Arg Ala Glu Tyr Leu Gly Ser Cys Leu Leu His
 170 175 180
 Lys Gly Tyr Lys Ser Ser Pro Asp Gln Phe Val Gly Ile Phe Ala
 185 190 195
 Gln Asn Arg Pro Glu Trp Ile Ile Ser Glu Leu Ala Cys Tyr Thr
 200 205 210
 Tyr Ser Met Val Ala Val Pro Leu Tyr Asp Thr Leu Gly Pro Glu
 215 220 225
 Ala Ile Val His Ile Val Asn Lys Ala Asp Ile Ala Met Val Ile
 230 235 240
 Cys Asp Thr Pro Gln Lys Ala Leu Val Leu Ile Gly Asn Val Glu
 245 250 255
 Lys Gly Phe Thr Pro Ser Leu Lys Val Ile Ile Leu Met Asp Pro
 260 265 270
 Phe Asp Asp Asp Leu Lys Gln Arg Gly Glu Lys Ser Gly Ile Glu
 275 280 285
 Ile Leu Ser Leu Tyr Asp Ala Glu Asn Leu Gly Lys Glu His Phe
 290 295 300
 Arg Lys Pro Val Pro Pro Ser Pro Glu Asp Leu Ser Val Ile Cys
 305 310 315
 Phe Thr Ser Gly Thr Thr Gly Asp Pro Lys Gly Ala Met Ile Thr

320	325	330
His Gln Asn Ile Val Ser Asn Ala Ala Ala	Phe Leu Lys Cys Val	
335	340	345
Glu His Ala Tyr Glu Pro Thr Pro Asp Asp	Val Ala Ile Ser Tyr	
350	355	360
Leu Pro Leu Ala His Met Phe Glu Arg Ile Val Gln Ala Val Val		
365	370	375
Tyr Ser Cys Gly Ala Arg Val Gly Phe Phe Gln Gly Asp Ile Arg		
380	385	390
Leu Leu Ala Asp Asp Met Lys Thr Leu Lys Pro Thr Leu Phe Pro		
395	400	405
Ala Val Pro Arg Leu Leu Asn Arg Ile Tyr Asp Lys Val Gln Asn		
410	415	420
Glu Ala Lys Thr Pro Leu Lys Lys Phe Leu Leu Lys Leu Ala Val		
425	430	435
Ser Ser Lys Phe Lys Glu Leu Gln Lys Gly Ile Ile Arg His Asp		
440	445	450
Ser Phe Trp Asp Lys Leu Ile Phe Ala Lys Ile Gln Asp Ser Leu		
455	460	465
Gly Gly Arg Val Arg Val Ile Val Thr Gly Ala Ala Pro Met Ser		
470	475	480
Thr Ser Val Met Thr Phe Phe Arg Ala Ala Met Gly Cys Gln Val		
485	490	495
Tyr Glu Ala Tyr Gly Gln Thr Glu Cys Thr Gly Gly Cys Thr Phe		
500	505	510
Thr Leu Pro Gly Asp Trp Thr Ser Gly His Val Gly Val Pro Leu		
515	520	525
Ala Cys Asn Tyr Val Lys Leu Glu Asp Val Ala Asp Met Asn Tyr		
530	535	540
Phe Thr Val Asn Asn Glu Gly Glu Val Cys Ile Lys Gly Thr Asn		
545	550	555
Val Phe Lys Gly Tyr Leu Lys Asp Pro Glu Lys Thr Gln Glu Ala		
560	565	570
Leu Asp Ser Asp Gly Trp Leu His Thr Gly Asp Ile Gly Arg Trp		
575	580	585
Leu Pro Asn Gly Thr Leu Lys Ile Ile Asp Arg Lys Lys Asn Ile		
590	595	600
Phe Lys Leu Ala Gln Gly Glu Tyr Ile Ala Pro Glu Lys Ile Glu		
605	610	615

Asn	Ile	Tyr	Asn	Arg	Ser	Gln	Pro	Val	Leu	Gln	Ile	Phe	Val	His
620									625					630
Gly	Glu	Ser	Leu	Arg	Ser	Ser	Leu	Val	Gly	Val	Val	Val	Pro	Asp
635								640					645	
Thr	Asp	Val	Leu	Pro	Ser	Phe	Ala	Ala	Lys	Leu	Gly	Val	Lys	Gly
650								655					660	
Ser	Phe	Glu	Glu	Leu	Cys	Gln	Asn	Gln	Val	Val	Arg	Glu	Ala	Ile
665								670					675	
Leu	Glu	Asp	Leu	Gln	Lys	Ile	Gly	Lys	Glu	Ser	Gly	Leu	Lys	Thr
680								685					690	
Phe	Glu	Gln	Val	Lys	Ala	Ile	Phe	Leu	His	Pro	Glu	Pro	Phe	Ser
695								700					705	
Ile	Glu	Asn	Gly	Leu	Leu	Thr	Pro	Thr	Leu	Lys	Ala	Lys	Arg	Gly
710								715					720	
Glu	Leu	Ser	Lys	Tyr	Phe	Arg	Thr	Gln	Ile	Asp	Ser	Leu	Tyr	Glu
725								730					735	
His Ile Gln Asp														

<210> 87
 <211> 2725
 <212> DNA
 <213> Homo sapiens

<400> 87
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 gcccggcg ggcccggggc ccctaagccca ttccctgaagt catggctgg 100
 ccaggacatt ggtgacccgc caatccggtt tggacgactg gaagcccagc 150
 cccctcatca agccctttgg ggctcggaag aagcggagct ggtaccttac 200
 ctggaagtat aaactgacaa accagcgggc cctgcggaga ttctgtcaga 250
 caggggccgt gctttcctg ctggtgactg tcattgtcaa tatcaagttg 300
 atcctggaca ctcggcgagc catcagtgaa gccaatgaag acccagagcc 350
 agagcaagac tatgatgagg ccctaggccc cctggagccc ccacggcgca 400
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 ccgggagcag ggccggggca tccatgtcat tgtcctcaac caggccacgg 550
 gcccacgtat ggcaaaacgt gtgtttgaca cgtactcacc tcatgaggat 600
 gaggccatgg tgctattcct caacatggta gcgccggcc gagtgctcat 650

ctgcactgtc aaggatgagg gtccttcca cctcaaggac acagccaagg 700
ctctgctgag gagcctggc agccaggctg gccctgcct gggctggagg 750
gacacatgg cttcgtgg acgaaaagga gtcctgtct tcggggagaa 800
acattctaag tcacctgccc tctttcctg gggggacca gtcctgctga 850
agacagatgt gccattgagc tcagcagaag aggcagagtg ccactggca 900
gacacagagc tgaaccgtcg ccgcggcgc ttctgcagca aagttgaggg 950
ctatggaagt gtatgcagct gcaaggaccc cacacccatc gagttcagcc 1000
ctgaccact cccagacaac aaggtcctca atgtcctgt ggctgtcatt 1050
gcagggAACc gacccaatta cctgtacagg atgctgcgt ctctgcttc 1100
agcccagggg gtgttcctc agatgataac agtttcatt gacggctact 1150
atgaggaacc catggatgtg gtggactgt ttggctgag gggcatccag 1200
catactccca tcagcatcaa gaatgccgc gtgtctcagc actacaaggc 1250
cagcctcact gccacttca acctgttcc ggaggccaag tttgctgtgg 1300
ttctggaaga ggacctggac attgctgtgg atttttcag tttcctgagc 1350
caatccatcc acctactgga ggaggatgac agcctgtact gcatctctgc 1400
ctggaatgac cagggatgt aacacacggc tgaggacca gcactactgt 1450
accgtgtgga gaccatgcct gggctggct gggctcag gaggtccttg 1500
tacaaggagg agctttagcc caagtggcct acaccggaa agctctggaa 1550
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tcatccctga cgccccga tcctaccact ttggcatcgt cggcctcaac 1650
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gttccaggt gtccagctca ggaatgtgga cagtctgaag aaagaagctt 1750
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gggggtcccc gcttccccct actcagtgaa gaagccaccc tcagtcaccc 2050
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cttagacact ggaccaggcc tcctctcagc cttcttttgc tccagatttc 2650
caaagctgga taagttggtc attgattaaa aaaggagaag ccctctggga 2700
aaaaaaaaaa aaaaaaaaaa aaaaaa 2725

<210> 88

<211> 660

<212> PRT

<213> Homo sapiens

<400> 88

Met Asp Asp Trp Lys Pro Ser Pro Leu Ile Lys Pro Phe Gly Ala
1 5 10 15

Arg Lys Lys Arg Ser Trp Tyr Leu Thr Trp Lys Tyr Lys Leu Thr
20 25 30

Asn Gln Arg Ala Leu Arg Arg Phe Cys Gln Thr Gly Ala Val Leu
35 40 45

Phe Leu Leu Val Thr Val Ile Val Asn Ile Lys Leu Ile Leu Asp
50 55 60

Thr Arg Arg Ala Ile Ser Glu Ala Asn Glu Asp Pro Glu Pro Glu
65 70 75

Gln Asp Tyr Asp Glu Ala Leu Gly Arg Leu Glu Pro Pro Arg Arg
80 85 90

Arg Gly Ser Gly Pro Arg Arg Val Leu Asp Val Glu Val Tyr Ser
95 100 105

Ser Arg Ser Lys Val Tyr Val Ala Val Asp Gly Thr Thr Val Leu
110 115 120

Glu Asp Glu Ala Arg Glu Gln Gly Arg Gly Ile His Val Ile Val
125 130 135

Leu Asn Gln Ala Thr Gly His Val Met Ala Lys Arg Val Phe Asp
 140 145 150
 Thr Tyr Ser Pro His Glu Asp Glu Ala Met Val Leu Phe Leu Asn
 155 160 165
 Met Val Ala Pro Gly Arg Val Leu Ile Cys Thr Val Lys Asp Glu
 170 175 180
 Gly Ser Phe His Leu Lys Asp Thr Ala Lys Ala Leu Leu Arg Ser
 185 190 195
 Leu Gly Ser Gln Ala Gly Pro Ala Leu Gly Trp Arg Asp Thr Trp
 200 205 210
 Ala Phe Val Gly Arg Lys Gly Gly Pro Val Phe Gly Glu Lys His
 215 220 225
 Ser Lys Ser Pro Ala Leu Ser Ser Trp Gly Asp Pro Val Leu Leu
 230 235 240
 Lys Thr Asp Val Pro Leu Ser Ser Ala Glu Glu Ala Glu Cys His
 245 250 255
 Trp Ala Asp Thr Glu Leu Asn Arg Arg Arg Arg Arg Phe Cys Ser
 260 265 270
 Lys Val Glu Gly Tyr Gly Ser Val Cys Ser Cys Lys Asp Pro Thr
 275 280 285
 Pro Ile Glu Phe Ser Pro Asp Pro Leu Pro Asp Asn Lys Val Leu
 290 295 300
 Asn Val Pro Val Ala Val Ile Ala Gly Asn Arg Pro Asn Tyr Leu
 305 310 315
 Tyr Arg Met Leu Arg Ser Leu Leu Ser Ala Gln Gly Val Ser Pro
 320 325 330
 Gln Met Ile Thr Val Phe Ile Asp Gly Tyr Tyr Glu Glu Pro Met
 335 340 345
 Asp Val Val Ala Leu Phe Gly Leu Arg Gly Ile Gln His Thr Pro
 350 355 360
 Ile Ser Ile Lys Asn Ala Arg Val Ser Gln His Tyr Lys Ala Ser
 365 370 375
 Leu Thr Ala Thr Phe Asn Leu Phe Pro Glu Ala Lys Phe Ala Val
 380 385 390
 Val Leu Glu Glu Asp Leu Asp Ile Ala Val Asp Phe Phe Ser Phe
 395 400 405
 Leu Ser Gln Ser Ile His Leu Leu Glu Glu Asp Asp Ser Leu Tyr
 410 415 420
 Cys Ile Ser Ala Trp Asn Asp Gln Gly Tyr Glu His Thr Ala Glu

425	430	435
Asp Pro Ala Leu Leu Tyr Arg Val Glu Thr Met Pro Gly Leu Gly		
440	445	450
Trp Val Leu Arg Arg Ser Leu Tyr Lys Glu Glu Leu Glu Pro Lys		
455	460	465
Trp Pro Thr Pro Glu Lys Leu Trp Asp Trp Asp Met Trp Met Arg		
470	475	480
Met Pro Glu Gln Arg Arg Gly Arg Glu Cys Ile Ile Pro Asp Val		
485	490	495
Ser Arg Ser Tyr His Phe Gly Ile Val Gly Leu Asn Met Asn Gly		
500	505	510
Tyr Phe His Glu Ala Tyr Phe Lys Lys His Lys Phe Asn Thr Val		
515	520	525
Pro Gly Val Gln Leu Arg Asn Val Asp Ser Leu Lys Lys Glu Ala		
530	535	540
Tyr Glu Val Glu Val His Arg Leu Leu Ser Glu Ala Glu Val Leu		
545	550	555
Asp His Ser Lys Asn Pro Cys Glu Asp Ser Phe Leu Pro Asp Thr		
560	565	570
Glu Gly His Thr Tyr Val Ala Phe Ile Arg Met Glu Lys Asp Asp		
575	580	585
Asp Phe Thr Thr Trp Thr Gln Leu Ala Lys Cys Leu His Ile Trp		
590	595	600
Asp Leu Asp Val Arg Gly Asn His Arg Gly Leu Trp Arg Leu Phe		
605	610	615
Arg Lys Lys Asn His Phe Leu Val Val Gly Val Pro Ala Ser Pro		
620	625	630
Tyr Ser Val Lys Lys Pro Pro Ser Val Thr Pro Ile Phe Leu Glu		
635	640	645
Pro Pro Pro Lys Glu Glu Gly Ala Pro Gly Ala Pro Glu Gln Thr		
650	655	660
<210> 89		
<211> 25		
<212> DNA		
<213> Artificial		
<220>		
<221> Artificial sequence		
<222> 1-25		
<223> Synthetic construct.		
<400> 89		

gatggcaaaa cgtgtgttg acacg 25

<210> 90
<211> 22
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-22
<223> Synthetic construct.

<400> 90
cctcaaccag gccacgggcc ac 22

<210> 91
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-24
<223> Synthetic construct.

<400> 91
cccaggcaga gatgcagtagtac aggc 24

<210> 92
<211> 26
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-26
<223> Synthetic construct.

<400> 92
cctccagtag gtggatggat tggctc 26

<210> 93
<211> 47
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-47
<223> Synthetic construct.

<400> 93
ctcacctcat gaggatgagg ccatggtgct attcctcaac atggtag 47

<210> 94
<211> 3037
<212> DNA
<213> Homo sapiens

<400> 94
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ctcttggAAC caccacaccc gtttaaagaa cctaagcacc atttaaagcc 100
actggaaatt tgggtctag tgggtgtgg tgaataaagg agggcagaat 150
ggatgatttc atctccatta gcctgctgTC tctggctatg ttgggtggat 200
gttacgtggc cggaaatcatt cccttggctg ttaatttctc agaggaacga 250
ctgaagctgg tgactgtttt gggtgctggc cttctctgtg gaactgctct 300
ggcagtcATC gtgcctgaag gagtacatgc cctttatgaa gatattttg 350
agggaaaaca ccaccaagca agtgaacac acataatgtat tgcatacagac 400
aaagcagcag aaaaatcaGT tggccatgaa catgagcaca gccacgacca 450
cacacagctg catgcctata ttgggtttc cctcgTTCTG ggcttcgttt 500
tcatgttgc ggtggaccag attggtaact cccatgtgc ttctactgac 550
gatccagaag cagcaaggTC tagcaattcc aaaatcacca ccacgctggg 600
tctggTTGTC catgctgcag ctgatgggt tgctttggc gcagcagcat 650
ctacttcaca gaccagtgtc cagttattt tgTTTgtggc aatcatgcta 700
cataaggcac cagctgCTT tggactggTT tccttcttga tgcatagtgg 750
cttagagcgg aatcaaatca gaaagcactt gctggTCTT gcattggcag 800
caccagttat gtccatggTG acataacttag gactgagtaa gagcagtaaa 850
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 <210> 95
 <211> 307
 <212> PRT
 <213> Homo sapiens

 <400> 95
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 Ser Glu Glu Arg Leu Lys Leu Val Thr Val Leu Gly Ala Gly Leu
 35 40 45

 Leu Cys Gly Thr Ala Leu Ala Val Ile Val Pro Glu Gly Val His
 50 55 60

 Ala Leu Tyr Glu Asp Ile Leu Glu Gly Lys His His Gln Ala Ser
 65 70 75

 Glu Thr His Asn Val Ile Ala Ser Asp Lys Ala Ala Glu Lys Ser
 80 85 90

 Val Val His Glu His Glu His Ser His Asp His Thr Gln Leu His
 95 100 105

 Ala Tyr Ile Gly Val Ser Leu Val Leu Gly Phe Val Phe Met Leu
 110 115 120

 Leu Val Asp Gln Ile Gly Asn Ser His Val His Ser Thr Asp Asp
 125 130 135

 Pro Glu Ala Ala Arg Ser Ser Asn Ser Lys Ile Thr Thr Thr Leu
 140 145 150

 Gly Leu Val Val His Ala Ala Ala Asp Gly Val Ala Leu Gly Ala
 155 160 165

 Ala Ala Ser Thr Ser Gln Thr Ser Val Gln Leu Ile Val Phe Val
 170 175 180

 Ala Ile Met Leu His Lys Ala Pro Ala Ala Phe Gly Leu Val Ser
 185 190 195

 Phe Leu Met His Ala Gly Leu Glu Arg Asn Arg Ile Arg Lys His
 200 205 210

 Leu Leu Val Phe Ala Leu Ala Ala Pro Val Met Ser Met Val Thr
 215 220 225

 Tyr Leu Gly Leu Ser Lys Ser Ser Lys Glu Ala Leu Ser Glu Val

230	235	240
Asn Ala Thr Gly Val Ala Met Leu Phe Ser Ala Gly Thr Phe Leu		
245	250	255
Tyr Val Ala Thr Val His Val Leu Pro Glu Val Gly Gly Ile Gly		
260	265	270
His Ser His Lys Pro Asp Ala Thr Gly Gly Arg Gly Leu Ser Arg		
275	280	285
Leu Glu Val Ala Ala Leu Val Leu Gly Cys Leu Ile Pro Leu Ile		
290	295	300
Leu Ser Val Gly His Gln His		
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<210> 96
<211> 25
<212> DNA
<213> Artificial

<220>
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<222> 1-25
<223> Synthetic construct.

<400> 96
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<210> 97
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-25
<223> Synthetic construct.

<400> 97
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<210> 98
<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-50
<223> Synthetic construct.

<400> 98
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<210> 99
<211> 1429

<212> DNA

<213> Homo sapiens

<400> 99

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ctgatttga gatgatgggc ttggaaacg ggcgtcgcag catgaagtcg 150
ccgcccctcg tgctggccgc cctgggtggcc tgcacatcg tcttggcctt 200
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<210> 100
<211> 401
<212> PRT
<213> Homo sapiens

<400> 100
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Asn Tyr Trp Ile Ala Ser Ser Arg Ser Val Asp Leu Gln Thr Arg
35 40 45

Ile Met Glu Leu Glu Gly Arg Val Arg Arg Ala Ala Ala Glu Arg
50 55 60

Gly Ala Val Glu Leu Lys Lys Asn Glu Phe Gln Gly Glu Leu Glu
65 70 75

Lys Gln Arg Glu Gln Leu Asp Lys Ile Gln Ser Ser His Asn Phe
80 85 90

Gln Leu Glu Ser Val Asn Lys Leu Tyr Gln Asp Glu Lys Ala Val
95 100 105

Leu Val Asn Asn Ile Thr Thr Gly Glu Arg Leu Ile Arg Val Leu
110 115 120

Gln Asp Gln Leu Lys Thr Leu Gln Arg Asn Tyr Gly Arg Leu Gln
125 130 135

Gln Asp Val Leu Gln Phe Gln Lys Asn Gln Thr Asn Leu Glu Arg
140 145 150

Lys Phe Ser Tyr Asp Leu Ser Gln Cys Ile Asn Gln Met Lys Glu
155 160 165

Val Lys Glu Gln Cys Glu Glu Arg Ile Glu Glu Val Thr Lys Lys
170 175 180

Gly Asn Glu Ala Val Ala Ser Arg Asp Leu Ser Glu Asn Asn Asp
185 190 195

Gln Arg Gln Gln Leu Gln Ala Leu Ser Glu Pro Gln Pro Arg Leu
200 205 210

Gln Ala Ala Gly Leu Pro His Thr Glu Val Pro Gln Gly Lys Gly
215 220 225

Asn Val Leu Gly Asn Ser Lys Ser Gln Thr Pro Ala Pro Ser Ser
230 235 240

Glu	Val	Val	Leu	Asp	Ser	Lys	Arg	Gln	Val	Glu	Lys	Glu	Glu	Thr
245									250					255
Asn	Glu	Ile	Gln	Val	Val	Asn	Glu	Glu	Pro	Gln	Arg	Asp	Arg	Leu
260									265					270
Pro	Gln	Glu	Pro	Gly	Arg	Glu	Gln	Val	Val	Glu	Asp	Arg	Pro	Val
275									280					285
Gly	Gly	Arg	Gly	Phe	Gly	Gly	Ala	Gly	Glu	Leu	Gly	Gln	Thr	Pro
290									295					300
Gln	Val	Gln	Ala	Ala	Leu	Ser	Val	Ser	Gln	Glu	Asn	Pro	Glu	Met
305									310					315
Glu	Gly	Pro	Glu	Arg	Asp	Gln	Leu	Val	Ile	Pro	Asp	Gly	Gln	Glu
320									325					330
Glu	Glu	Gln	Glu	Ala	Ala	Gly	Glu	Gly	Arg	Asn	Gln	Gln	Lys	Leu
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Arg	Gly	Glu	Asp	Asp	Tyr	Asn	Met	Asp	Glu	Asn	Glu	Ala	Glu	Ser
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Glu	Thr	Asp	Lys	Gln	Ala	Ala	Leu	Ala	Gly	Asn	Asp	Arg	Asn	Ile
365									370					375
Asp	Val	Phe	Asn	Val	Glu	Asp	Gln	Lys	Arg	Asp	Thr	Ile	Asn	Leu
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<210> 101

<211> 3671

<212> DNA

<213> Homo sapiens

<400> 101

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<210> 102

<211> 1089

<212> PRT

<213> Homo sapiens

<400> 102

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					20				25				30	
Thr	Arg	Leu	Glu	Leu	Thr	Asn	His	Ser	Ser	Cys	Gln	Glu	Pro	Pro
					35				40				45	
Gly	Pro	Gly	Ser	Leu	Pro	Trp	Gly	Ser	Gln	Gly	Lys	Pro	Gly	Ala
				50				55				60		
Cys	Trp	Met	Ala	Ser	Arg	Phe	Ser	Arg	Val	Val	Leu	Val	Ile	
					65				70				75	
Asp	Ala	Leu	Arg	Phe	Asp	Phe	Ala	Gln	Pro	Gln	His	Ser	His	Val
				80				85				90		
Pro	Arg	Glu	Pro	Pro	Val	Ser	Leu	Pro	Phe	Leu	Gly	Lys	Leu	Ser
					95				100				105	
Ser	Leu	Gln	Arg	Ile	Leu	Glu	Ile	Gln	Pro	His	His	Ala	Arg	Leu
				110				115				120		
Tyr	Arg	Ser	Gln	Val	Asp	Pro	Pro	Thr	Thr	Thr	Met	Gln	Arg	Leu
				125				130				135		
Lys	Ala	Leu	Thr	Thr	Gly	Ser	Leu	Pro	Thr	Phe	Ile	Asp	Ala	Gly
				140				145				150		
Ser	Asn	Phe	Ala	Ser	His	Ala	Ile	Val	Glu	Asp	Asn	Leu	Ile	Lys
					155				160				165	
Gln	Leu	Thr	Ser	Ala	Gly	Arg	Arg	Val	Val	Phe	Met	Gly	Asp	Asp
					170				175				180	
Thr	Trp	Lys	Asp	Leu	Phe	Pro	Gly	Ala	Phe	Ser	Lys	Ala	Phe	Phe
					185				190				195	
Phe	Pro	Ser	Phe	Asn	Val	Arg	Asp	Leu	Asp	Thr	Val	Asp	Asn	Gly

200	205	210
Ile Leu Glu His Leu Tyr Pro Thr Met	Asp Ser Gly Glu Trp Asp	
215	220	225
Val Leu Ile Ala His Phe Leu Gly Val	Asp His Cys Gly His Lys	
230	235	240
His Gly Pro His His Pro Glu Met Ala	Lys Lys Leu Ser Gln Met	
245	250	255
Asp Gln Val Ile Gln Gly Leu Val Glu	Arg Leu Glu Asn Asp Thr	
260	265	270
Leu Leu Val Val Ala Gly Asp His Gly	Met Thr Thr Asn Gly Asp	
275	280	285
His Gly Gly Asp Ser Glu Leu Glu Val	Ser Ala Ala Leu Phe Leu	
290	295	300
Tyr Ser Pro Thr Ala Val Phe Pro Ser	Thr Pro Pro Glu Glu Pro	
305	310	315
Glu Val Ile Pro Gln Val Ser Leu Val	Pro Thr Leu Ala Leu Leu	
320	325	330
Leu Gly Leu Pro Ile Pro Phe Gly Asn	Ile Gly Glu Val Met Ala	
335	340	345
Glu Leu Phe Ser Gly Gly Glu Asp Ser	Gln Pro His Ser Ser Ala	
350	355	360
Leu Ala Gln Ala Ser Ala Leu His Leu	Asn Ala Gln Gln Val Ser	
365	370	375
Arg Phe Leu His Thr Tyr Ser Ala Ala	Thr Gln Asp Leu Gln Ala	
380	385	390
Lys Glu Leu His Gln Leu Gln Asn Leu	Phe Ser Lys Ala Ser Ala	
395	400	405
Asp Tyr Gln Trp Leu Leu Gln Ser Pro	Lys Gly Ala Glu Ala Thr	
410	415	420
Leu Pro Thr Val Ile Ala Glu Leu Gln	Gln Phe Leu Arg Gly Ala	
425	430	435
Arg Ala Met Cys Ile Glu Ser Trp Ala	Arg Phe Ser Leu Val Arg	
440	445	450
Met Ala Gly Gly Thr Ala Leu Leu Ala	Ala Ser Cys Phe Ile Cys	
455	460	465
Leu Leu Ala Ser Gln Trp Ala Ile Ser	Pro Gly Phe Pro Phe Cys	
470	475	480
Pro Leu Leu Leu Thr Pro Val Ala Trp	Gly Leu Val Gly Ala Ile	
485	490	495

Ala Tyr Ala Gly Leu Leu Gly Thr Ile Glu Leu Lys Leu Asp Leu
 500 505 510
 Val Leu Leu Gly Ala Val Ala Val Ser Ser Phe Leu Pro Phe
 515 520 525
 Leu Trp Lys Ala Trp Ala Gly Trp Gly Ser Lys Arg Pro Leu Ala
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 Thr Leu Phe Pro Ile Pro Gly Pro Val Leu Leu Leu Leu Leu Phe
 545 550 555
 Arg Leu Ala Val Phe Phe Ser Asp Ser Phe Val Val Ala Glu Ala
 560 565 570
 Arg Ala Thr Pro Phe Leu Leu Gly Ser Phe Ile Leu Leu Leu Val
 575 580 585
 Val Gln Leu His Trp Glu Gly Gln Leu Leu Pro Pro Lys Leu Leu
 590 595 600
 Thr Met Pro Arg Leu Gly Thr Ser Ala Thr Thr Asn Pro Pro Arg
 605 610 615
 His Asn Gly Ala Tyr Ala Leu Arg Leu Gly Ile Gly Leu Leu Leu
 620 625 630
 Cys Thr Arg Leu Ala Gly Leu Phe His Arg Cys Pro Glu Glu Thr
 635 640 645
 Pro Val Cys His Ser Ser Pro Trp Leu Ser Pro Leu Ala Ser Met
 650 655 660
 Val Gly Gly Arg Ala Lys Asn Leu Trp Tyr Gly Ala Cys Val Ala
 665 670 675
 Ala Leu Val Ala Leu Leu Ala Ala Val Arg Leu Trp Leu Arg Arg
 680 685 690
 Tyr Gly Asn Leu Lys Ser Pro Glu Pro Pro Met Leu Phe Val Arg
 695 700 705
 Trp Gly Leu Pro Leu Met Ala Leu Gly Thr Ala Ala Tyr Trp Ala
 710 715 720
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 725 730 735
 Val Ser Gly Ala Ser Met Val Leu Pro Arg Ala Val Ala Gly Leu
 740 745 750
 Ala Ala Ser Gly Leu Ala Leu Leu Leu Trp Lys Pro Val Thr Val
 755 760 765
 Leu Val Lys Ala Gly Ala Gly Ala Pro Arg Thr Arg Thr Val Leu
 770 775 780
 Thr Pro Phe Ser Gly Pro Pro Thr Ser Gln Ala Asp Leu Asp Tyr

785	790	795
Val Val Pro Gln Ile Tyr Arg His Met Gln	Glu Glu Phe Arg	Gly
800	805	810
Arg Leu Glu Arg Thr Lys Ser Gln Gly	Pro Leu Thr Val Ala Ala	
815	820	825
Tyr Gln Leu Gly Ser Val Tyr Ser Ala Ala	Met Val Thr Ala Leu	
830	835	840
Thr Leu Leu Ala Phe Pro Leu Leu Leu	Leu His Ala Glu Arg Ile	
845	850	855
Ser Leu Val Phe Leu Leu Phe Leu Gln	Ser Phe Leu Leu	Leu
860	865	870
His Leu Leu Ala Ala Gly Ile Pro Val	Thr Thr Pro Gly Pro Phe	
875	880	885
Thr Val Pro Trp Gln Ala Val Ser Ala	Trp Ala Leu Met Ala Thr	
890	895	900
Gln Thr Phe Tyr Ser Thr Gly His Gln	Pro Val Phe Pro Ala Ile	
905	910	915
His Trp His Ala Ala Phe Val Gly Phe	Pro Glu Gly His Gly Ser	
920	925	930
Cys Thr Trp Leu Pro Ala Leu Val Gly	Ala Asn Thr Phe Ala	
935	940	945
Ser His Leu Leu Phe Ala Val Gly Cys	Pro Leu Leu Leu Leu Trp	
950	955	960
Pro Phe Leu Cys Glu Ser Gln Gly Leu	Arg Lys Arg Gln Gln Pro	
965	970	975
Pro Gly Asn Glu Ala Asp Ala Arg Val	Arg Pro Glu Glu Glu	
980	985	990
Glu Pro Leu Met Glu Met Arg Leu Arg	Asp Ala Pro Gln His Phe	
995	1000	1005
Tyr Ala Ala Leu Leu Gln Leu Gly	Leu Lys Tyr Leu Phe Ile Leu	
1010	1015	1020
Gly Ile Gln Ile Leu Ala Cys Ala Leu	Ala Ala Ser Ile Leu Arg	
1025	1030	1035
Arg His Leu Met Val Trp Lys Val Phe	Ala Pro Lys Phe Ile Phe	
1040	1045	1050
Glu Ala Val Gly Phe Ile Val Ser Ser	Val Gly Leu Leu Leu Gly	
1055	1060	1065
Ile Ala Leu Val Met Arg Val Asp Gly	Ala Val Ser Ser Trp Phe	
1070	1075	1080

Arg Gln Leu Phe Leu Ala Gln Gln Arg
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<210> 103

<211> 1743

<212> DNA

<213> Homo sapiens

<400> 103

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cttatccatc aacatgaaga atgtcctaca atggactcca ccagagggtc 150
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cccaccagag gtggcactga ctacagatga gaagtccatt tctgttgcc 250
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taaatcaaac agaacgtggt cccagtgtgt gaccaaccac acgctgggtc 400
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<210> 104

<211> 442

<212> PRT

<213> Homo sapiens

<400> 104

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Leu	Leu	Thr	Leu	Cys	Ser	Ile	Ser	Ser	Gln	Ile	Gly	Pro	Pro	Glu
				20					25				30	
Val	Ala	Leu	Thr	Thr	Asp	Glu	Lys	Ser	Ile	Ser	Val	Val	Leu	Thr
					35				40				45	
Ala	Pro	Glu	Lys	Trp	Lys	Arg	Asn	Pro	Glu	Asp	Leu	Pro	Val	Ser
				50				55				60		
Met	Gln	Gln	Ile	Tyr	Ser	Asn	Leu	Lys	Tyr	Asn	Val	Ser	Val	Leu
				65					70				75	
Asn	Thr	Lys	Ser	Asn	Arg	Thr	Trp	Ser	Gln	Cys	Val	Thr	Asn	His
				80				85				90		
Thr	Leu	Val	Leu	Thr	Trp	Leu	Glu	Pro	Asn	Thr	Leu	Tyr	Cys	Val
				95				100				105		
His	Val	Glu	Ser	Phe	Val	Pro	Gly	Pro	Pro	Arg	Arg	Ala	Gln	Pro
				110				115				120		
Ser	Glu	Lys	Gln	Cys	Ala	Arg	Thr	Leu	Lys	Asp	Gln	Ser	Ser	Glu
				125					130				135	
Phe	Lys	Ala	Lys	Ile	Ile	Phe	Trp	Tyr	Val	Leu	Pro	Ile	Ser	Ile
				140				145				150		
Thr	Val	Phe	Leu	Phe	Ser	Val	Met	Gly	Tyr	Ser	Ile	Tyr	Arg	Tyr
				155				160				165		

Ile His Val Gly Lys Glu Lys His Pro Ala Asn Leu Ile Leu Ile
 170 175 180
 Tyr Gly Asn Glu Phe Asp Lys Arg Phe Phe Val Pro Ala Glu Lys
 185 190 195
 Ile Val Ile Asn Phe Ile Thr Leu Asn Ile Ser Asp Asp Ser Lys
 200 205 210
 Ile Ser His Gln Asp Met Ser Leu Leu Gly Lys Ser Ser Asp Val
 215 220 225
 Ser Ser Leu Asn Asp Pro Gln Pro Ser Gly Asn Leu Arg Pro Pro
 230 235 240
 Gln Glu Glu Glu Glu Val Lys His Leu Gly Tyr Ala Ser His Leu
 245 250 255
 Met Glu Ile Phe Cys Asp Ser Glu Glu Asn Thr Glu Gly Thr Ser
 260 265 270
 Leu Thr Gln Gln Glu Ser Leu Ser Arg Thr Ile Pro Pro Asp Lys
 275 280 285
 Thr Val Ile Glu Tyr Glu Tyr Asp Val Arg Thr Thr Asp Ile Cys
 290 295 300
 Ala Gly Pro Glu Glu Gln Glu Leu Ser Leu Gln Glu Glu Val Ser
 305 310 315
 Thr Gln Gly Thr Leu Leu Glu Ser Gln Ala Ala Leu Ala Val Leu
 320 325 330
 Gly Pro Gln Thr Leu Gln Tyr Ser Tyr Thr Pro Gln Leu Gln Asp
 335 340 345
 Leu Asp Pro Leu Ala Gln Glu His Thr Asp Ser Glu Glu Gly Pro
 350 355 360
 Glu Glu Glu Pro Ser Thr Thr Leu Val Asp Trp Asp Pro Gln Thr
 365 370 375
 Gly Arg Leu Cys Ile Pro Ser Leu Ser Ser Phe Asp Gln Asp Ser
 380 385 390
 Glu Gly Cys Glu Pro Ser Glu Gly Asp Gly Leu Gly Glu Glu Gly
 395 400 405
 Leu Leu Ser Arg Leu Tyr Glu Glu Pro Ala Pro Asp Arg Pro Pro
 410 415 420
 Gly Glu Asn Glu Thr Tyr Leu Met Gln Phe Met Glu Glu Trp Gly
 425 430 435
 Leu Tyr Val Gln Met Glu Asn
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<210> 105

<211> 21
<212> DNA
<213> Artificial

<220>
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<222> 1-21
<223> Synthetic construct

<400> 105
cgctgctgct gttgctcctg g 21

<210> 106
<211> 18
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 106
cagtgtgc ca ggactttg 18

<210> 107
<211> 18
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 107
agtgcgcaggc agcgttgg 18

<210> 108
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-25
<223> Synthetic construct.

<400> 108
ctcctccgag tctgtgtc cctgc 25

<210> 109
<211> 51
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence

<222> 1-51
<223> Synthetic construct.

<400> 109
ggacgggcag ttccctgtgt ctctggtgtt ttgcctaaac ctgcaaacat 50
c 51

<210> 110
<211> 1114
<212> DNA
<213> Homo sapiens

<400> 110
cgacgcgtg ggcggacgcg tggcggacg cgtgggtctc tgcggggaga 50
cgccagcctg cgtctgccat gggctcggg ttgaggggtt ggggacgtcc 100
tctgctgact gtggccaccg ccctgatgct gccgtgaag ccccccgcag 150
gctcctgggg ggccagatc atcgggggcc acgaggtgac ccccccactcc 200
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aaaaaaaaaa gaaa 1114

<210> 111

<211> 283

<212> PRT

<213> Homo sapiens

<400> 111

Met Gly Leu Gly Leu Arg Gly Trp Gly Arg Pro Leu Leu Thr Val
1 5 10 15

Ala Thr Ala Leu Met Leu Pro Val Lys Pro Pro Ala Gly Ser Trp
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Gly Ala Gln Ile Ile Gly Gly His Glu Val Thr Pro His Ser Arg
35 40 45

Pro Tyr Met Ala Ser Val Arg Phe Gly Gly Gln His His Cys Gly
50 55 60

Gly Phe Leu Leu Arg Ala Arg Trp Val Val Ser Ala Ala His Cys
65 70 75

Phe Ser His Arg Asp Leu Arg Thr Gly Leu Val Val Leu Gly Ala
80 85 90

His Val Leu Ser Thr Ala Glu Pro Thr Gln Gln Val Phe Gly Ile
95 100 105

Asp Ala Leu Thr Thr His Pro Asp Tyr His Pro Met Thr His Ala
110 115 120

Asn Asp Ile Cys Leu Leu Arg Leu Asn Gly Ser Ala Val Leu Gly
125 130 135

Pro Ala Val Gly Leu Leu Arg Leu Pro Gly Arg Arg Ala Arg Pro
140 145 150

Pro Thr Ala Gly Thr Arg Cys Arg Val Ala Gly Trp Gly Phe Val
155 160 165

Ser Asp Phe Glu Glu Leu Pro Pro Gly Leu Met Glu Ala Lys Val
170 175 180

Arg Val Leu Asp Pro Asp Val Cys Asn Ser Ser Trp Lys Gly His
185 190 195

Leu Thr Leu Thr Met Leu Cys Thr Arg Ser Gly Asp Ser His Arg
200 205 210

Arg Gly Phe Cys Ser Ala Asp Ser Gly Gly Pro Leu Val Cys Arg
215 220 225

Asn Arg Ala His Gly Leu Val Ser Phe Ser Gly Leu Trp Cys Gly
230 235 240

Asp Pro Lys Thr Pro Asp Val Tyr Thr Gln Val Ser Ala Phe Val
245 250 255

Ala Trp Ile Trp Asp Val Val Arg Arg Ser Ser Pro Gln Pro Gly
260 265 270

Pro Leu Pro Gly Thr Thr Arg Pro Pro Gly Glu Ala Ala
275 280

<210> 112
<211> 24
<212> DNA
<213> Artificial

<220>
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<222> 1-24
<223> Synthetic construct.

<400> 112
gacgtctgca acagctcctg gaag 24

<210> 113
<211> 23
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-23
<223> Synthetic construct.

<400> 113
cgagaaggaa acgaggccgt gag 23

<210> 114
<211> 44
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-44
<223> Synthetic construct.

<400> 114
tgacacttac catgctctgc acccgcaagt gggacagcca caga 44

<210> 115
<211> 1808
<212> DNA
<213> Homo sapiens

<400> 115
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<210> 116
 <211> 331
 <212> PRT
 <213> Homo sapiens

<400> 116
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Gly Ala Ala Val Leu Leu Lys Asp Tyr Val Thr Gly Gly Ala Cys
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Pro Ser Lys Ala Thr Ile Pro Gly Lys Thr Val Ile Val Thr Gly
 35 40 45

Ala Asn Thr Gly Ile Gly Lys Gln Thr Ala Leu Glu Leu Ala Arg
 50 55 60

Arg Gly Gly Asn Ile Ile Leu Ala Cys Arg Asp Met Glu Lys Cys
 65 70 75

Glu Ala Ala Ala Lys Asp Ile Arg Gly Glu Thr Leu Asn His His
 80 85 90

Val Asn Ala Arg His Leu Asp Leu Ala Ser Leu Lys Ser Ile Arg
 95 100 105

Glu Phe Ala Ala Lys Ile Ile Glu Glu Glu Glu Arg Val Asp Ile
 110 115 120

Leu Ile Asn Asn Ala Gly Val Met Arg Cys Pro His Trp Thr Thr
 125 130 135

Glu Asp Gly Phe Glu Met Gln Phe Gly Val Asn His Leu Gly His
 140 145 150

Phe Leu Leu Thr Asn Leu Leu Leu Asp Lys Leu Lys Ala Ser Ala
 155 160 165

Pro Ser Arg Ile Ile Asn Leu Ser Ser Leu Ala His Val Ala Gly
 170 175 180

His Ile Asp Phe Asp Asp Leu Asn Trp Gln Thr Arg Lys Tyr Asn
 185 190 195

Thr Lys Ala Ala Tyr Cys Gln Ser Lys Leu Ala Ile Val Leu Phe
 200 205 210

Thr Lys Glu Leu Ser Arg Arg Leu Gln Gly Ser Gly Val Thr Val
 215 220 225

Asn Ala Leu His Pro Gly Val Ala Arg Thr Glu Leu Gly Arg His
230 235 240
Thr Gly Ile His Gly Ser Thr Phe Ser Ser Thr Thr Leu Gly Pro
245 250 255
Ile Phe Trp Leu Leu Val Lys Ser Pro Glu Leu Ala Ala Gln Pro
260 265 270
Ser Thr Tyr Leu Ala Val Ala Glu Glu Leu Ala Asp Val Ser Gly
275 280 285
Lys Tyr Phe Asp Gly Leu Lys Gln Lys Ala Pro Ala Pro Glu Ala
290 295 300
Glu Asp Glu Glu Val Ala Arg Arg Leu Trp Ala Glu Ser Ala Arg
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Leu Val Gly Leu Glu Ala Pro Ser Val Arg Glu Gln Pro Leu Pro
320 325 330

Arg

<210> 117
<211> 2249
<212> DNA
<213> Homo sapiens

<400> 117
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 <210> 118
 <211> 544
 <212> PRT
 <213> Homo sapiens
 <400> 118
 Met Gly Pro Gly Ala Arg Leu Ala Ala Leu Leu Ala Val Leu Ala
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 Leu Gly Thr Gly Asp Pro Glu Arg Ala Ala Ala Arg Gly Asp Thr
 20 25 30
 Phe Ser Ala Leu Thr Ser Val Ala Arg Ala Leu Ala Pro Glu Arg
 35 40 45
 Arg Leu Leu Gly Leu Leu Arg Arg Tyr Leu Arg Gly Glu Glu Ala
 50 55 60
 Arg Leu Arg Asp Leu Thr Arg Phe Tyr Asp Lys Val Leu Ser Leu
 65 70 75
 His Glu Asp Ser Thr Thr Pro Val Ala Asn Pro Leu Leu Ala Phe
 80 85 90
 Thr Leu Ile Lys Arg Leu Gln Ser Asp Trp Arg Asn Val Val His
 95 100 105
 Ser Leu Glu Ala Ser Glu Asn Ile Arg Ala Leu Lys Asp Gly Tyr
 110 115 120
 Glu Lys Val Glu Gln Asp Leu Pro Ala Phe Glu Asp Leu Glu Gly
 125 130 135
 Ala Ala Arg Ala Leu Met Arg Leu Gln Asp Val Tyr Met Leu Asn
 140 145 150
 Val Lys Gly Leu Ala Arg Gly Val Phe Gln Arg Val Thr Gly Ser
 155 160 165
 Ala Ile Thr Asp Leu Tyr Ser Pro Lys Arg Leu Phe Ser Leu Thr
 170 175 180
 Gly Asp Asp Cys Phe Gln Val Gly Lys Val Ala Tyr Asp Met Gly
 185 190 195
 Asp Tyr Tyr His Ala Ile Pro Trp Leu Glu Glu Ala Val Ser Leu
 200 205 210
 Phe Arg Gly Ser Tyr Gly Glu Trp Lys Thr Glu Asp Glu Ala Ser
 215 220 225
 Leu Glu Asp Ala Leu Asp His Leu Ala Phe Ala Tyr Phe Arg Ala
 230 235 240

Gly Asn Val Ser Cys Ala Leu Ser Leu Ser Arg Glu Phe Leu Leu
 245 250 255
 Tyr Ser Pro Asp Asn Lys Arg Met Ala Arg Asn Val Leu Lys Tyr
 260 265 270
 Glu Arg Leu Leu Ala Glu Ser Pro Asn His Val Val Ala Glu Ala
 275 280 285
 Val Ile Gln Arg Pro Asn Ile Pro His Leu Gln Thr Arg Asp Thr
 290 295 300
 Tyr Glu Gly Leu Cys Gln Thr Leu Gly Ser Gln Pro Thr Leu Tyr
 305 310 315
 Gln Ile Pro Ser Leu Tyr Cys Ser Tyr Glu Thr Asn Ser Asn Ala
 320 325 330
 Tyr Leu Leu Leu Gln Pro Ile Arg Lys Glu Val Ile His Leu Glu
 335 340 345
 Pro Tyr Ile Ala Leu Tyr His Asp Phe Val Ser Asp Ser Glu Ala
 350 355 360
 Gln Lys Ile Arg Glu Leu Ala Glu Pro Trp Leu Gln Arg Ser Val
 365 370 375
 Val Ala Ser Gly Glu Lys Gln Leu Gln Val Glu Tyr Arg Ile Ser
 380 385 390
 Lys Ser Ala Trp Leu Lys Asp Thr Val Asp Pro Lys Leu Val Thr
 395 400 405
 Leu Asn His Arg Ile Ala Ala Leu Thr Gly Leu Asp Val Arg Pro
 410 415 420
 Pro Tyr Ala Glu Tyr Leu Gln Val Val Asn Tyr Gly Ile Gly Gly
 425 430 435
 His Tyr Glu Pro His Phe Asp His Ala Thr Ser Pro Ser Ser Pro
 440 445 450
 Leu Tyr Arg Met Lys Ser Gly Asn Arg Val Ala Thr Phe Met Ile
 455 460 465
 Tyr Leu Ser Ser Val Glu Ala Gly Gly Ala Thr Ala Phe Ile Tyr
 470 475 480
 Ala Asn Leu Ser Val Pro Val Val Arg Asn Ala Ala Leu Phe Trp
 485 490 495
 Trp Asn Leu His Arg Ser Gly Glu Gly Asp Ser Asp Thr Leu His
 500 505 510
 Ala Gly Cys Pro Val Leu Val Gly Asp Lys Trp Val Ala Asn Lys
 515 520 525
 Trp Ile His Glu Tyr Gly Gln Glu Phe Arg Arg Pro Cys Ser Ser

530

535

540

Ser Pro Glu Asp

<210> 119

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 119

cgggacagga gaccagaaa ggg 23

<210> 120

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 120

ggccaagtga tccaaggcat cttc 24

<210> 121

<211> 49

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-49

<223> Synthetic construct.

<400> 121

ctgcgggacc tgacttagatt ctacgacaag gtactttctt tgcattggg 49

<210> 122

<211> 1778

<212> DNA

<213> Homo sapiens

<400> 122

gagataggga gtctgggttt aagttcctgc tccatctcag gagccctgc 50

tcccacccct aggaagccac cagactccac ggtgtgggc caatcaggtg 100

gaatcggccc tggcaggtgg ggccacgagc gctggctgag ggaccgagcc 150

ggagagcccc ggagcccccg taaccgcgc gggagcgcc caggatgccg 200

cgcgccccact cgaggcaggc gcgcgtactgc gcgcgttct cctacccctg 250
gctcaagttt tcacttatca tctattccac cgtgttctgg ctgattgggg 300
ccctggtcct gtctgtggc atctatgcag aggttgagcg gcagaaatat 350
aaaacccttgc aaagtgcctt cctggctcca gccatcatcc tcatccctc 400
gggcgtcgcc atgttcatgg tctccttcat tgggtgtgctg gcgtccctcc 450
gtgacaacct gtaccccttc caagcattca tgtacatcct tgggatctgc 500
ctcatcatgg agctcattgg tggcgtggtg gcctgacct tccggaaacca 550
gaccattgac ttccctgaacg acaacattcg aagaggaatt gagaactact 600
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tccttgagcc tagttttttt ttacgtgatt tttgttaacat tcattttttt 1650

gtacagataa caggagtttc tgactaatca aagctggtat ttcccccgtat 1700
gtcttattct tgcccttccc ccaaccagtt tgttaatcaa acaataaaaa 1750
catgttttgtt tttgtttta aaaaaaaaa 1778

<210> 123
<211> 294
<212> PRT
<213> Homo sapiens

<400> 123

Met	Pro	Arg	Gly	Asp	Ser	Glu	Gln	Val	Arg	Tyr	Cys	Ala	Arg	Phe
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Ser	Tyr	Leu	Trp	Leu	Lys	Phe	Ser	Leu	Ile	Ile	Tyr	Ser	Thr	Val
				20					25					30
Phe	Trp	Leu	Ile	Gly	Ala	Leu	Val	Leu	Ser	Val	Gly	Ile	Tyr	Ala
				35					40					45
Glu	Val	Glu	Arg	Gln	Lys	Tyr	Lys	Thr	Leu	Glu	Ser	Ala	Phe	Leu
				50					55					60
Ala	Pro	Ala	Ile	Ile	Leu	Ile	Leu	Leu	Gly	Val	Val	Met	Phe	Met
				65					70					75
Val	Ser	Phe	Ile	Gly	Val	Leu	Ala	Ser	Leu	Arg	Asp	Asn	Leu	Tyr
				80					85					90
Leu	Leu	Gln	Ala	Phe	Met	Tyr	Ile	Leu	Gly	Ile	Cys	Leu	Ile	Met
				95					100					105
Glu	Leu	Ile	Gly	Gly	Val	Val	Ala	Leu	Thr	Phe	Arg	Asn	Gln	Thr
				110					115					120
Ile	Asp	Phe	Leu	Asn	Asp	Asn	Ile	Arg	Arg	Gly	Ile	Glu	Asn	Tyr
				125					130					135
Tyr	Asp	Asp	Leu	Asp	Phe	Lys	Asn	Ile	Met	Asp	Phe	Val	Gln	Lys
				140					145					150
Lys	Phe	Lys	Cys	Cys	Gly	Gly	Glu	Asp	Tyr	Arg	Asp	Trp	Ser	Lys
				155					160					165
Asn	Gln	Tyr	His	Asp	Cys	Ser	Ala	Pro	Gly	Pro	Leu	Ala	Cys	Gly
				170					175					180
Val	Pro	Tyr	Thr	Cys	Cys	Ile	Arg	Asn	Thr	Thr	Glu	Val	Val	Asn
				185					190					195
Thr	Met	Cys	Gly	Tyr	Lys	Thr	Ile	Asp	Lys	Glu	Arg	Phe	Ser	Val
				200					205					210
Gln	Asp	Val	Ile	Tyr	Val	Arg	Gly	Cys	Thr	Asn	Ala	Val	Ile	Ile
				215					220					225
Trp	Phe	Met	Asp	Asn	Tyr	Thr	Ile	Met	Ala	Cys	Ile	Leu	Leu	Gly

230	235	240
Ile Leu Leu Pro Gln Phe Leu Gly Val Leu Leu Thr Leu Leu Tyr		
245	250	255
Ile Thr Arg Val Glu Asp Ile Ile Met Glu His Ser Val Thr Asp		
260	265	270
Gly Leu Leu Gly Pro Gly Ala Lys Pro Ser Val Glu Ala Ala Gly		
275	280	285
Thr Gly Cys Cys Leu Cys Tyr Pro Asn		
290		

<210> 124
 <211> 25
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-25
 <223> Synthetic construct.

<400> 124
 atcatctatt ccaccgtgtt ctggc 25

<210> 125
 <211> 25
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-25
 <223> Synthetic construct.

<400> 125
 gacagaggtgc tccatgtatga tgtcc 25

<210> 126
 <211> 50
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-50
 <223> Synthetic construct.

<400> 126
 cctgtctgtg ggcatctatg cagaggttga gcggcagaaa tataaaaaccc 50

<210> 127
 <211> 1636
 <212> DNA
 <213> Homo sapiens

<400> 127
gaggagcggg ccgaggactc cagcgtgccc aggtctggca tcctgcactt 50
gctgccctct gacacctggg aagatggccg gcccgtggac cttcaccctt 100
ctctgtggtt tgctggcagc caccttgcac caagccaccc tcagtcac 150
tgcagttctc atcctcggcc caaaagtcat caaagaaaag ctgacacagg 200
agctgaagga ccacaacgccc accagcatcc tgacgcagct gcccgtgctc 250
agtgcacatgc gggaaaagcc agccggaggc atccctgtgc tggcagcct 300
ggtgaacacc gtcctgaagc acatcatctg gctgaaggctc atcacagcta 350
acatcctcca gctgcaggtg aagccctcg ccaatgacca ggagctgcta 400
gtcaagatcc ccctggacat ggtggctgaa ttcaacacgc ccctggtaa 450
gaccatcgatg gagttccaca tgacgactga ggcccaagcc accatccgca 500
tggacaccag tgcaagtggc cccacccgccc tggcctcag tgactgtgcc 550
accagccatg ggagcctgac catccaactg ctgtataagc ttccttcct 600
ggtaacgcc ttagctaagc aggtcatgaa cctccttagt ccattccctgc 650
ccaatctagt gaaaaaccag ctgtgtcccg tgatcgagggc ttcccttaat 700
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ccattcagct ctacccctggg gccaagttgt tggactcaca gggaaagggtg 850
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caacatcccg ttcaagcctca tcgtgagtc gtagctggtg aaagctgcag 950
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atgaactctg ggattggctg gttccaaacct gatgttctga aaaacatcat 1350
cactgagatc atccactcca tcctgctgcc gaaccagaat ggcaaattaa 1400
gatctgggtt cccagtgta ttggtaagg ccttggatt cgaggcagct 1450

gagtcctcac tgaccaagga tgcccttgc cttactccag ctccttgc 1500
gaaacccagc tctcctgtct cccagtgaag acttggatgg cagccatcg 1550
ggaaggctgg gtcccagctg ggagtatggg tgtgagctct atagaccatc 1600
cctctctgca atcaataaac acttgcctgt gaaaaa 1636

<210> 128

<211> 484

<212> PRT

<213> Homo sapiens

<400> 128

Met	Ala	Gly	Pro	Trp	Thr	Phe	Thr	Leu	Leu	Cys	Gly	Leu	Leu	Ala
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Ala	Thr	Leu	Ile	Gln	Ala	Thr	Leu	Ser	Pro	Thr	Ala	Val	Leu	Ile
		20						25						30
Leu	Gly	Pro	Lys	Val	Ile	Lys	Glu	Lys	Leu	Thr	Gln	Glu	Leu	Lys
			35					40						45
Asp	His	Asn	Ala	Thr	Ser	Ile	Leu	Gln	Gln	Leu	Pro	Leu	Leu	Ser
				50				55						60
Ala	Met	Arg	Glu	Lys	Pro	Ala	Gly	Gly	Ile	Pro	Val	Leu	Gly	Ser
				65				70						75
Leu	Val	Asn	Thr	Val	Leu	Lys	His	Ile	Ile	Trp	Leu	Lys	Val	Ile
				80				85						90
Thr	Ala	Asn	Ile	Leu	Gln	Leu	Gln	Val	Lys	Pro	Ser	Ala	Asn	Asp
				95				100						105
Gln	Glu	Leu	Leu	Val	Lys	Ile	Pro	Leu	Asp	Met	Val	Ala	Gly	Phe
				110				115						120
Asn	Thr	Pro	Leu	Val	Lys	Thr	Ile	Val	Glu	Phe	His	Met	Thr	Thr
				125				130						135
Glu	Ala	Gln	Ala	Thr	Ile	Arg	Met	Asp	Thr	Ser	Ala	Ser	Gly	Pro
				140				145						150
Thr	Arg	Leu	Val	Leu	Ser	Asp	Cys	Ala	Thr	Ser	His	Gly	Ser	Leu
				155				160						165
Arg	Ile	Gln	Leu	Leu	Tyr	Lys	Leu	Ser	Phe	Leu	Val	Asn	Ala	Leu
				170				175						180
Ala	Lys	Gln	Val	Met	Asn	Leu	Leu	Val	Pro	Ser	Leu	Pro	Asn	Leu
				185				190						195
Val	Lys	Asn	Gln	Leu	Cys	Pro	Val	Ile	Glu	Ala	Ser	Phe	Asn	Gly
				200				205						210
Met	Tyr	Ala	Asp	Leu	Leu	Gln	Leu	Val	Lys	Val	Pro	Ile	Ser	Leu
				215				220						225

Ser Ile Asp Arg Leu Glu Phe Asp Leu Leu Tyr Pro Ala Ile Lys
 230 235 240
 Gly Asp Thr Ile Gln Leu Tyr Leu Gly Ala Lys Leu Leu Asp Ser
 245 250 255
 Gln Gly Lys Val Thr Lys Trp Phe Asn Asn Ser Ala Ala Ser Leu
 260 265 270
 Thr Met Pro Thr Leu Asp Asn Ile Pro Phe Ser Leu Ile Val Ser
 275 280 285
 Gln Asp Val Val Lys Ala Ala Val Ala Ala Val Leu Ser Pro Glu
 290 295 300
 Glu Phe Met Val Leu Leu Asp Ser Val Leu Pro Glu Ser Ala His
 305 310 315
 Arg Leu Lys Ser Ser Ile Gly Leu Ile Asn Glu Lys Ala Ala Asp
 320 325 330
 Lys Leu Gly Ser Thr Gln Ile Val Lys Ile Leu Thr Gln Asp Thr
 335 340 345
 Pro Glu Phe Phe Ile Asp Gln Gly His Ala Lys Val Ala Gln Leu
 350 355 360
 Ile Val Leu Glu Val Phe Pro Ser Ser Glu Ala Leu Arg Pro Leu
 365 370 375
 Phe Thr Leu Gly Ile Glu Ala Ser Ser Glu Ala Gln Phe Tyr Thr
 380 385 390
 Lys Gly Asp Gln Leu Ile Leu Asn Leu Asn Asn Ile Ser Ser Asp
 395 400 405
 Arg Ile Gln Leu Met Asn Ser Gly Ile Gly Trp Phe Gln Pro Asp
 410 415 420
 Val Leu Lys Asn Ile Ile Thr Glu Ile Ile His Ser Ile Leu Leu
 425 430 435
 Pro Asn Gln Asn Gly Lys Leu Arg Ser Gly Val Pro Val Ser Leu
 440 445 450
 Val Lys Ala Leu Gly Phe Glu Ala Ala Glu Ser Ser Leu Thr Lys
 455 460 465
 Asp Ala Leu Val Leu Thr Pro Ala Ser Leu Trp Lys Pro Ser Ser
 470 475 480
 Pro Val Ser Gln

<210> 129
 <211> 2213
 <212> DNA
 <213> Homo sapiens

<400> 129
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gtggtggcgc tgctcatcgt ttgcgacgtt ccctcagcct ctgccaaag 100
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ctaacaaaag acctgtaata agaatgaatg gagacaagtt ccgtcgccct 200
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ccaaacgggg tgatacatat gagttacagg tgcggggttt ttcagctgag 500
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aactactact ttgttttagt tagaacaag ctcaaaacta ctttagttaa 1350
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aaaaaaaaaa aaa 2213

<210> 130

<211> 335

<212> PRT

<213> Homo sapiens

<400> 130

Met	Ala	Ala	Arg	Trp	Arg	Phe	Trp	Cys	Val	Ser	Val	Thr	Met	Val
1				5					10				15	

Val	Ala	Leu	Leu	Ile	Val	Cys	Asp	Val	Pro	Ser	Ala	Ser	Ala	Gln
				20				25					30	

Arg	Lys	Lys	Glu	Met	Val	Leu	Ser	Glu	Lys	Val	Ser	Gln	Leu	Met
				35				40				45		

Glu	Trp	Thr	Asn	Lys	Arg	Pro	Val	Ile	Arg	Met	Asn	Gly	Asp	Lys
	50							55				60		

Phe	Arg	Arg	Leu	Val	Lys	Ala	Pro	Pro	Arg	Asn	Tyr	Ser	Val	Ile
			65					70				75		

Val	Met	Phe	Thr	Ala	Leu	Gln	Leu	His	Arg	Gln	Cys	Val	Val	Cys
	80							85				90		

Lys	Gln	Ala	Asp	Glu	Glu	Phe	Gln	Ile	Leu	Ala	Asn	Ser	Trp	Arg
			95					100				105		

Tyr Ser Ser Ala Phe Thr Asn Arg Ile Phe Phe Ala Met Val Asp
 110 115 120
 Phe Asp Glu Gly Ser Asp Val Phe Gln Met Leu Asn Met Asn Ser
 125 130 135
 Ala Pro Thr Phe Ile Asn Phe Pro Ala Lys Gly Lys Pro Lys Arg
 140 145 150
 Gly Asp Thr Tyr Glu Leu Gln Val Arg Gly Phe Ser Ala Glu Gln
 155 160 165
 Ile Ala Arg Trp Ile Ala Asp Arg Thr Asp Val Asn Ile Arg Val
 170 175 180
 Ile Arg Pro Pro Asn Tyr Ala Gly Pro Leu Met Leu Gly Leu Leu
 185 190 195
 Leu Ala Val Ile Gly Gly Leu Val Tyr Leu Arg Arg Ser Asn Met
 200 205 210
 Glu Phe Leu Phe Asn Lys Thr Gly Trp Ala Phe Ala Ala Leu Cys
 215 220 225
 Phe Val Leu Ala Met Thr Ser Gly Gln Met Trp Asn His Ile Arg
 230 235 240
 Gly Pro Pro Tyr Ala His Lys Asn Pro His Thr Gly His Val Asn
 245 250 255
 Tyr Ile His Gly Ser Ser Gln Ala Gln Phe Val Ala Glu Thr His
 260 265 270
 Ile Val Leu Leu Phe Asn Gly Gly Val Thr Leu Gly Met Val Leu
 275 280 285
 Leu Cys Glu Ala Ala Thr Ser Asp Met Asp Ile Gly Lys Arg Lys
 290 295 300
 Ile Met Cys Val Ala Gly Ile Gly Leu Val Val Leu Phe Phe Ser
 305 310 315
 Trp Met Leu Ser Ile Phe Arg Ser Lys Tyr His Gly Tyr Pro Tyr
 320 325 330
 Ser Phe Leu Met Ser
 335

<210> 131
 <211> 2476
 <212> DNA
 <213> Homo sapiens

<400> 131
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tcagaaccgc taccggcgat gctactgctg tgggtgtcgg tggtcgcagc 150
cttggcgctg gcggtaactgg ccccccggagc aggggagcag aggcggagag 200
cagccaaagc gcccaatgtg gtgctggtcg tgagcgactc cttcgatgga 250
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ctttatgaag acacgtggaa cttccttct gaatgcctac acaaactctc 350
caatttgttgc cccatcacgc gcagcaatgt ggagtggcct cttcactcac 400
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agaatacaga caaagcagta aactggtaa gaaaggaagc aattaattac 700
actgaaccat ttgttattta ctgggattta aatttaccac acccttaccc 750
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attnaaagccg gcctacaagt atcaaatgtg gtttcttttg tggatattta 1200
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gatactctt gttggcgatca tcattcggaaa catttaagaa tgaacataaa 1300
gtcaaaaacc tgcatccacc ctggattctg agtgaattcc atggatgtaa 1350
tgtgaatgcc tccacccatac tgcttcgaac taaccactgg aaatataatag 1400
cctattcgga tggtgcatca atattgcctc aactcttgc tcttcctcg 1450
gatccagatg aattaacaaa tggatgttgc aaatttccag aaattactta 1500
ttctttggat cagaagcttc attccattat aaactaccct aaagttctg 1550

cttctgtcca ccagtataat aaagagcagt ttatcaagtg gaaacaaagt 1600
ataggacaga attattcaaa cgttatagca aatcttaggt ggcaccaaga 1650
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acctgtatc ccagacttt gggaggctga ggaaagcaga tcacaaggc 1900
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<210> 132

<211> 536

<212> PRT

<213> Homo sapiens

<400> 132

Met	Leu	Leu	Leu	Trp	Val	Ser	Val	Val	Ala	Ala	Leu	Ala	Leu	Ala
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Val	Leu	Ala	Pro	Gly	Ala	Gly	Glu	Gln	Arg	Arg	Arg	Ala	Ala	Lys
								20		25			30	
Ala	Pro	Asn	Val	Val	Leu	Val	Val	Ser	Asp	Ser	Phe	Asp	Gly	Arg
									35		40		45	
Leu	Thr	Phe	His	Pro	Gly	Ser	Gln	Val	Val	Lys	Leu	Pro	Phe	Ile
								50		55		60		
Asn	Phe	Met	Lys	Thr	Arg	Gly	Thr	Ser	Phe	Leu	Asn	Ala	Tyr	Thr
								65		70		75		

Asn	Ser	Pro	Ile	Cys	Cys	Pro	Ser	Arg	Ala	Ala	Met	Trp	Ser	Gly
80														90
Leu	Phe	Thr	His	Leu	Thr	Glu	Ser	Trp	Asn	Asn	Phe	Lys	Gly	Leu
95														105
Asp	Pro	Asn	Tyr	Thr	Thr	Trp	Met	Asp	Val	Met	Glu	Arg	His	Gly
110														120
Tyr	Arg	Thr	Gln	Lys	Phe	Gly	Lys	Leu	Asp	Tyr	Thr	Ser	Gly	His
125														135
His	Ser	Ile	Ser	Asn	Arg	Val	Glu	Ala	Trp	Thr	Arg	Asp	Val	Ala
140														150
Phe	Leu	Leu	Arg	Gln	Glu	Gly	Arg	Pro	Met	Val	Asn	Leu	Ile	Arg
155														165
Asn	Arg	Thr	Lys	Val	Arg	Val	Met	Glu	Arg	Asp	Trp	Gln	Asn	Thr
170														180
Asp	Lys	Ala	Val	Asn	Trp	Leu	Arg	Lys	Glu	Ala	Ile	Asn	Tyr	Thr
185														195
Glu	Pro	Phe	Val	Ile	Tyr	Leu	Gly	Leu	Asn	Leu	Pro	His	Pro	Tyr
200														210
Pro	Ser	Pro	Ser	Ser	Gly	Glu	Asn	Phe	Gly	Ser	Ser	Thr	Phe	His
215														225
Thr	Ser	Leu	Tyr	Trp	Leu	Glu	Lys	Val	Ser	His	Asp	Ala	Ile	Lys
230														240
Ile	Pro	Lys	Trp	Ser	Pro	Leu	Ser	Glu	Met	His	Pro	Val	Asp	Tyr
245														255
Tyr	Ser	Ser	Tyr	Thr	Lys	Asn	Cys	Thr	Gly	Arg	Phe	Thr	Lys	Lys
260														270
Glu	Ile	Lys	Asn	Ile	Arg	Ala	Phe	Tyr	Tyr	Ala	Met	Cys	Ala	Glu
275														285
Thr	Asp	Ala	Met	Leu	Gly	Glu	Ile	Ile	Leu	Ala	Leu	His	Gln	Leu
290														300
Asp	Leu	Leu	Gln	Lys	Thr	Ile	Val	Ile	Tyr	Ser	Ser	Asp	His	Gly
305														315
Glu	Leu	Ala	Met	Glu	His	Arg	Gln	Phe	Tyr	Lys	Met	Ser	Met	Tyr
320														330
Glu	Ala	Ser	Ala	His	Val	Pro	Leu	Leu	Met	Met	Gly	Pro	Gly	Ile
335														345
Lys	Ala	Gly	Leu	Gln	Val	Ser	Asn	Val	Val	Ser	Leu	Val	Asp	Ile
350														360
Tyr	Pro	Thr	Met	Leu	Asp	Ile	Ala	Gly	Ile	Pro	Leu	Pro	Gln	Asn

365	370	375
Leu Ser Gly Tyr Ser Leu Leu Pro Leu	Ser Ser Glu Thr Phe Lys	
380	385	390
Asn Glu His Lys Val Lys Asn Leu His	Pro Pro Trp Ile Leu Ser	
395	400	405
Glu Phe His Gly Cys Asn Val Asn Ala	Ser Thr Tyr Met Leu Arg	
410	415	420
Thr Asn His Trp Lys Tyr Ile Ala Tyr	Ser Asp Gly Ala Ser Ile	
425	430	435
Leu Pro Gln Leu Phe Asp Leu Ser Ser	Asp Pro Asp Glu Leu Thr	
440	445	450
Asn Val Ala Val Lys Phe Pro Glu Ile	Thr Tyr Ser Leu Asp Gln	
455	460	465
Lys Leu His Ser Ile Ile Asn Tyr Pro	Lys Val Ser Ala Ser Val	
470	475	480
His Gln Tyr Asn Lys Glu Gln Phe Ile	Lys Trp Lys Gln Ser Ile	
485	490	495
Gly Gln Asn Tyr Ser Asn Val Ile Ala	Asn Leu Arg Trp His Gln	
500	505	510
Asp Trp Gln Lys Glu Pro Arg Lys Tyr	Glu Asn Ala Ile Asp Gln	
515	520	525
Trp Leu Lys Thr His Met Asn Pro Arg	Ala Val	
530	535	

<210> 133
 <211> 1475
 <212> DNA
 <213> Homo sapiens

<400> 133
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 gtttctactg agaggtctgc catggcctct cttggcctcc aacttgtgg 150
 ctacatccta ggccttctgg ggctttggg cacactggtt gccatgctgc 200
 tccccagctg gaaaacaagt tcttatgtcg gtgccagcat tgtgacagca 250
 gttggcttct ccaaggccct ctggatggaa tgtgccacac acagcacagg 300
 catcacccag tgtgacatct atagcacctt tctggcctg cccgctgaca 350
 tccaggctgc ccaggccatg atggtgacat ccagtgcaat ctcctccctg 400
 gcctgcatta tctctgtggt gggcatgaga tgcacagtct tctgccagga 450

atcccgagcc aaagacagag tggcggtagc aggtggagtc ttttcatcc 500
ttggaggcct cctgggattc attcctgttgcctgaaatct tcatgggatc 550
ctacgggact tctactcacc actggtgctt gacagcatga aatttgagat 600
tggagaggct cttaacttgg gcattatttc ttccctgttc tccctgatag 650
ctggaatcat cctctgcttt tcctgctcat cccagagaaa tcgctccaac 700
tactacgatg cctaccaagc ccaaccttgc cccacaagga gctctccaag 750
gcctggtcaa cctcccaaag tcaagagtga gttcaattcc tacagcctga 800
cagggtatgt gtgaagaacc aggggccaga gctgggggtt ggctgggtct 850
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gcagcctggg acatttaaaa aaata 1475

<210> 134

<211> 230

<212> PRT

<213> Homo sapiens

<400> 134

Met Ala Ser Leu Gly Leu Gln Leu Val Gly Tyr Ile Leu Gly Leu
1 5 10 15

Leu Gly Leu Leu Gly Thr Leu Val Ala Met Leu Leu Pro Ser Trp
20 25 30

Lys Thr Ser Ser Tyr Val Gly Ala Ser Ile Val Thr Ala Val Gly
35 40 45

Phe Ser Lys Gly Leu Trp Met Glu Cys Ala Thr His Ser Thr Gly

50	55	60
Ile Thr Gln Cys Asp Ile Tyr Ser Thr Leu Leu Gly Leu Pro Ala		
65	70	75
Asp Ile Gln Ala Ala Gln Ala Met Met Val Thr Ser Ser Ala Ile		
80	85	90
Ser Ser Leu Ala Cys Ile Ile Ser Val Val Gly Met Arg Cys Thr		
95	100	105
Val Phe Cys Gln Glu Ser Arg Ala Lys Asp Arg Val Ala Val Ala		
110	115	120
Gly Gly Val Phe Phe Ile Leu Gly Gly Leu Leu Gly Phe Ile Pro		
125	130	135
Val Ala Trp Asn Leu His Gly Ile Leu Arg Asp Phe Tyr Ser Pro		
140	145	150
Leu Val Pro Asp Ser Met Lys Phe Glu Ile Gly Glu Ala Leu Tyr		
155	160	165
Leu Gly Ile Ile Ser Ser Leu Phe Ser Leu Ile Ala Gly Ile Ile		
170	175	180
Leu Cys Phe Ser Cys Ser Ser Gln Arg Asn Arg Ser Asn Tyr Tyr		
185	190	195
Asp Ala Tyr Gln Ala Gln Pro Leu Ala Thr Arg Ser Ser Pro Arg		
200	205	210
Pro Gly Gln Pro Pro Lys Val Lys Ser Glu Phe Asn Ser Tyr Ser		
215	220	225
Leu Thr Gly Tyr Val		
230		
<210> 135		
<211> 610		
<212> DNA		
<213> Homo sapiens		
<400> 135		
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aagtcatcgc tcccgctggc tcagaaccat ggctgtgcca gccggcaccc 150		
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cgccatcgtg tccctgagcg agacccgcca atgtggtccc ccctgcaccc 250		
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gattttgttg tgaagctgaa gttcagggt gtgaattccc agtgccactc 350		

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acatagaaag aaaatcaact ttcactaagg catctcagaa acataggcta 450
aggtaatatg tgtaccagta gagaagcctg aggaatttac aaaatgatgc 500
agctccaagc cattgtatgg cccatgtggg agactgatgg gacatggaga 550
atgacagtag attatcagga aataaataaa gtggttttc caatgtacac 600
acctgtaaaa 610

<210> 136
<211> 119
<212> PRT
<213> Homo sapiens

<400> 136

Met	Val	Pro	Arg	Ile	Phe	Ala	Pro	Ala	Tyr	Val	Ser	Val	Cys	Leu
1					5					10				15

Leu Leu Leu Cys Pro Arg Glu Val Ile Ala Pro Ala Gly Ser Glu
20 25 30

Pro Trp Leu Cys Gln Pro Ala Pro Arg Cys Gly Asp Lys Ile Tyr
35 40 45

Asn Pro Leu Glu Gln Cys Cys Tyr Asn Asp Ala Ile Val Ser Leu
50 55 60

Ser Glu Thr Arg Gln Cys Gly Pro Pro Cys Thr Phe Trp Pro Cys
65 70 75

Phe Glu Leu Cys Cys Leu Asp Ser Phe Gly Leu Thr Asn Asp Phe
80 85 90

Val Val Lys Leu Lys Val Gln Gly Val Asn Ser Gln Cys His Ser
95 100 105

Ser Pro Ile Ser Ser Lys Cys Glu Ser Arg Arg Arg Phe Pro
110 115 ..

<210> 137
<211> 771
<212> DNA
<213> Homo sapiens

<400> 137

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gtggggacaa gttctacgac cccctgcagc actgttgcta tcatgtatgcc 200
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agctaattgga acatcagggg aacgatgact cctggattct cttcctggg 400
tgggcctgga gaaagaggct ggtgttacct gagatctggg atgctgagtg 450
gctgtttggg ggccagagaa acacacactc aactgcccac ttcattctgt 500
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tatgtacttt ataaatgaaa a 771

<210> 138

<211> 110

<212> PRT

<213> Homo sapiens.

<400> 138

Met Ala Pro Arg Gly Cys Ile Val Ala Val Phe Ala Ile Phe Cys
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Ile Ser Arg Leu Leu Cys Ser His Gly Ala Pro Val Ala Pro Met
20 25 30

Thr Pro Tyr Leu Met Leu Cys Gln Pro His Lys Arg Cys Gly Asp
35 40 45

Lys Phe Tyr Asp Pro Leu Gln His Cys Cys Tyr Asp Asp Ala Val
50 55 60

Val Pro Leu Ala Arg Thr Gln Thr Cys Gly Asn Cys Thr Phe Arg
65 70 75

Val Cys Phe Glu Gln Cys Cys Pro Trp Thr Phe Met Val Lys Leu
80 85 90

Ile Asn Gln Asn Cys Asp Ser Ala Arg Thr Ser Asp Asp Arg Leu
95 100 105

Cys Arg Ser Val Ser
110

<210> 139

<211> 2044

<212> DNA

<213> Homo sapiens

<400> 139

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cccacggccc tggaggccgg cagctggcgc tggggatccc tgctttcgc 200
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gacgtggtac cgcaagtcga gggcgaggt gcagacctgc tcagagcgcc 400
ggcccatccg caaccctcag ttccaggacc ttcacctgca ccatggaggc 450
caccaggctg ccaacaccag ccacgacctg gtcagcgcc acgggctgga 500
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ctccccactgc tcagcgcggg ccattgcaag ggtgccacac aatgtcttgt 1950
ccaccctggg acacttctga gtatgaagcg ggatgctatt aaaaactaca 2000
tggggaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaga 2044

<210> 140

<211> 311

<212> PRT

<213> Homo sapiens

<400> 140

Met Gly Val Pro Thr Ala Leu Glu Ala Gly Ser Trp Arg Trp Gly
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Ser Leu Leu Phe Ala Leu Phe Leu Ala Ala Ser Leu Gly Pro Val
20 25 30

Ala Ala Phe Lys Val Ala Thr Pro Tyr Ser Leu Tyr Val Cys Pro
35 40 45

Glu Gly Gln Asn Val Thr Leu Thr Cys Arg Leu Leu Gly Pro Val
50 55 .. 60

Asp Lys Gly His Asp Val Thr Phe Tyr Lys Thr Trp Tyr Arg Ser
65 70 75

Ser Arg Gly Glu Val Gln Thr Cys Ser Glu Arg Arg Pro Ile Arg
80 85 90

Asn Leu Thr Phe Gln Asp Leu His Leu His His Gly Gly His Gln
95 100 105

Ala Ala Asn Thr Ser His Asp Leu Ala Gln Arg His Gly Leu Glu
110 115 120

Ser Ala Ser Asp His His Gly Asn Phe Ser Ile Thr Met Arg Asn
125 130 135

Leu Thr Leu Leu Asp Ser Gly Leu Tyr Cys Cys Leu Val Val Glu

140	145	150
Ille Arg His His His Ser Glu His Arg Val His Gly Ala Met Glu		
155	160	165
Leu Gln Val Gln Thr Gly Lys Asp Ala Pro Ser Asn Cys Val Val		
170	175	180
Tyr Pro Ser Ser Ser Gln Asp Ser Glu Asn Ile Thr Ala Ala Ala		
185	190	195
Leu Ala Thr Gly Ala Cys Ile Val Gly Ile Leu Cys Leu Pro Leu		
200	205	210
Ille Leu Leu Leu Val Tyr Lys Gln Arg Gln Ala Ala Ser Asn Arg		
215	220	225
Arg Ala Gln Glu Leu Val Arg Met Asp Ser Asn Ile Gln Gly Ile		
230	235	240
Glu Asn Pro Gly Phe Glu Ala Ser Pro Pro Ala Gln Gly Ile Pro		
245	250	255
Glu Ala Lys Val Arg His Pro Leu Ser Tyr Val Ala Gln Arg Gln		
260	265	270
Pro Ser Glu Ser Gly Arg His Leu Leu Ser Glu Pro Ser Thr Pro		
275	280	285
Leu Ser Pro Pro Gly Pro Gly Asp Val Phe Phe Pro Ser Leu Asp		
290	295	300
Pro Val Pro Asp Ser Pro Asn Phe Glu Val Ile		
305	310	

<210> 141
 <211> 1732
 <212> DNA
 <213> Homo sapiens

<400> 141
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 tctgtggccc ctgtgcctcc gtgtccttt cgtctccctt cttcccgact 250
 ccgctccgg accagcggcc tgaccctgg gaaaggatgg ttcccggatgt 300
 gagggtcctc tcctccctgc tggactcgc gctgctctgg ttccccctgg 350
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 agataactccc ccggcgagag ctggcacccc tacttggagc cacaaggcct 450

gatgtactgc ctgcgctgta cctgctcaga gggcgccat gtgagttgtt 500
accgcctcca ctgtccgcct gtccactgcc cccagcctgt gacggagcca 550
cagcaatgtc gtcccaagtg tgtggAACCT cacactccct ctggactccg 600
ggccccacca aagtccctgcc agcacaacgg gaccatgtac caacacggag 650
agatcttcag tgcccatgag ctgttcccct cccgcctgcc caaccagtgt 700
gtcctctgca gctgcacaga gggccagatc tactgcggcc tcacaacctg 750
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aagcctgcaa agatgaggca agtgagcaat cgatgaaaga ggacagtgtg 850
cagtcgctcc atgggttgag acatcctcag gatccatgtt ccagtgtgc 900
tgggagaaag agaggcccgg gcaccccagc ccccactggc ctcagcgccc 950
ctctgagctt catccctcgc cacttcagac ccaagggagc aggcagcaca 1000
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cggaagacg tactcccacg gggaggtgtg gcacccggcc ttccgtgcct 1100
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ggccagtcca gacaaagtga ccaagacata acaaagacct aacagttgca 1650
gatatgagct gtataattgt tgTTTattata tattaataaa taagaagttg 1700
cattaccctc aaaaaaaaaa aaaaaaaaaa aa 1732

<210> 142
<211> 451
<212> PRT
<213> Homo sapiens

<400> 142

Met Val Pro Glu Val Arg Val Leu Ser Ser Leu Leu Gly Leu Ala
 1 5 10 15
 Leu Leu Trp Phe Pro Leu Asp Ser His Ala Arg Ala Arg Pro Asp
 20 25 30
 Met Phe Cys Leu Phe His Gly Lys Arg Tyr Ser Pro Gly Glu Ser
 35 40 45
 Trp His Pro Tyr Leu Glu Pro Gln Gly Leu Met Tyr Cys Leu Arg
 50 55 60
 Cys Thr Cys Ser Glu Gly Ala His Val Ser Cys Tyr Arg Leu His
 65 70 75
 Cys Pro Pro Val His Cys Pro Gln Pro Val Thr Glu Pro Gln Gln
 80 85 90
 Cys Cys Pro Lys Cys Val Glu Pro His Thr Pro Ser Gly Leu Arg
 95 100 105
 Ala Pro Pro Lys Ser Cys Gln His Asn Gly Thr Met Tyr Gln His
 110 115 120
 Gly Glu Ile Phe Ser Ala His Glu Leu Phe Pro Ser Arg Leu Pro
 125 130 135
 Asn Gln Cys Val Leu Cys Ser Cys Thr Glu Gly Gln Ile Tyr Cys
 140 145 150
 Gly Leu Thr Thr Cys Pro Glu Pro Gly Cys Pro Ala Pro Leu Pro
 155 160 165
 Leu Pro Asp Ser Cys Cys Gln Ala Cys Lys Asp Glu Ala Ser Glu
 170 175 180
 Gln Ser Asp Glu Glu Asp Ser Val Gln Ser Leu His Gly Val Arg
 185 190 195
 His Pro Gln Asp Pro Cys Ser Ser Asp Ala Gly Arg Lys Arg Gly
 200 205 210
 Pro Gly Thr Pro Ala Pro Thr Gly Leu Ser Ala Pro Leu Ser Phe
 215 220 225
 Ile Pro Arg His Phe Arg Pro Lys Gly Ala Gly Ser Thr Thr Val
 230 235 240
 Lys Ile Val Leu Lys Glu Lys His Lys Lys Ala Cys Val His Gly
 245 250 255
 Gly Lys Thr Tyr Ser His Gly Glu Val Trp His Pro Ala Phe Arg
 260 265 270
 Ala Phe Gly Pro Leu Pro Cys Ile Leu Cys Thr Cys Glu Asp Gly
 275 280 285
 Arg Gln Asp Cys Gln Arg Val Thr Cys Pro Thr Glu Tyr Pro Cys

290	295	300
Arg His Pro Glu Lys Val Ala Gly Lys Cys Cys Lys Ile Cys Pro		
305	310	315
Glu Asp Lys Ala Asp Pro Gly His Ser Glu Ile Ser Ser Thr Arg		
320	325	330
Cys Pro Lys Ala Pro Gly Arg Val Leu Val His Thr Ser Val Ser		
335	340	345
Pro Ser Pro Asp Asn Leu Arg Arg Phe Ala Leu Glu His Glu Ala		
350	355	360
Ser Asp Leu Val Glu Ile Tyr Leu Trp Lys Leu Val Lys Asp Glu		
365	370	375
Glu Thr Glu Ala Gln Arg Gly Glu Val Pro Gly Pro Arg Pro His		
380	385	390
Ser Gln Asn Leu Pro Leu Asp Ser Asp Gln Glu Ser Gln Glu Ala		
395	400	405
Arg Leu Pro Glu Arg Gly Thr Ala Leu Pro Thr Ala Arg Trp Pro		
410	415	420
Pro Arg Arg Ser Leu Glu Arg Leu Pro Ser Pro Asp Pro Gly Ala		
425	430	435
Glu Gly His Gly Gln Ser Arg Gln Ser Asp Gln Asp Ile Thr Lys		
440	445	450

Thr

<210> 143
<211> 693
<212> DNA
<213> Homo sapiens

<400> 143
ctagcctgcg ccaagggtta gtgagaccgc gggcaacag cttgcggctg 50
cggggagctc ccgtggcgc tccgctggct gtgcaggcgg ccatggattc 100
cttgcggaaa atgctgatct cagtcgaat gctggcgca gggctggcg 150
tgggctacgc gtcctcggt atcgtgaccc cggagagcg gcgaaagcag 200
gaaatgctaa aggagatgcc actgcaggac ccaaggagca gggaggaggc 250
ggccaggacc cagcagctat tgctggccac tctgcaggag gcagcgcacca 300
cgcaggagaa cgtggcctgg aggaagaact ggtgggtgg cggcgaaggc 350
ggcgccagcg ggaggtcacc gtgagaccgg acttgcctcc gtggcgccg 400
gaccttggct tggcgcagg aatccgaggc agccttctc cttcgtggc 450

ccagcggaga gtccggaccg agataccatg ccaggactct ccggggtcct 500
gtgagctgcc gtcgggtgag cacgttccc ccaaaccctg gactgactgc 550
tttaaggccc gcaaggcggg ccagggccga gacgcgagtc ggatgtggtg 600
aactgaaaga accaataaaa tcatgttcct ccaaaaaaaaaaaaaaaa 650
aaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa aaa 693

<210> 144
<211> 93
<212> PRT
<213> Homo sapiens

<400> 144
Met Asp Ser Leu Arg Lys Met Leu Ile Ser Val Ala Met Leu Gly
1 5 10 15
Ala Gly Ala Gly Val Gly Tyr Ala Leu Leu Val Ile Val Thr Pro
20 25 30
Gly Glu Arg Arg Lys Gln Glu Met Leu Lys Glu Met Pro Leu Gln
35 40 45
Asp Pro Arg Ser Arg Glu Glu Ala Ala Arg Thr Gln Gln Leu Leu
50 55 60
Leu Ala Thr Leu Gln Glu Ala Ala Thr Thr Gln Glu Asn Val Ala
65 70 75
Trp Arg Lys Asn Trp Met Val Gly Gly Glu Gly Gly Ala Ser Gly
80 85 90
Arg Ser Pro

<210> 145
<211> 1883
<212> DNA
<213> Homo sapiens

<400> 145
caggagagaa ggcaccgccc ccaccccgcc tccaaagcta accctcgggc 50
ttgaggggaa gaggctgact gtacgttcct tctactctgg caccactctc 100
caggctgcca tggggcccaag caccctctc ctcatcttgt tcctttgtc 150
atggtcggga cccctccaag gacagcagca ccaccttgg gagtacatgg 200
aacgcccact agctgcttta gaggaacggc tggcccagtg ccaggaccag 250
agtagtcggc atgctgctga gctgcggac ttcaagaaca agatgctgcc 300
actgctggag gtggcagaga aggagcggga ggcactcaga actgaggccg 350
acaccatctc cgggagagtg gatcgtctgg agcgggaggt agactatctg 400

gagacccaga acccagctct gccctgtgta gagtttgatg agaaggtgac 450
tggaggccct gggaccaaag gcaagggaag aaggaatgag aagtacgata 500
tggtgacaga ctgtggctac acaatctctc aagttagatc aatgaagatt 550
ctgaagcgat ttggtgccc agctggctta tggaccaagg atccactggg 600
gcaaacagag aagatcta^{cg} tgtagatgg gacacagaat gacacagcct 650
ttgtcttccc aaggctgcgt gacttcaccc ttgccatggc tgcccgaaa 700
gcttcccgag tccgggtgcc cttccctgg gtaggcacag ggcagctgg 750
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gaggtggtga gatggagaac actttgcagc taatcaaatt ccacctggca 850
aaccgaacag tggtggacag ctcagtattc ccagcagagg ggctgatccc 900
cccctacggc ttgacagcag acacctacat cgacctggta gctgatgagg 950
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ctggccaagt tagatccaca gacactggac acagagcagc agtgggacac 1050
accatgtccc agagagaatg ctgaggctgc ctttgcatac tgtgggaccc 1100
tctatgtcgt ctataacacc cgtcctgcca gtcgggccc catccagtgc 1150
tcctttgatg ccagccgcac cctgaccctt gaacggcag cactccctta 1200
ttttccccgc agatatggtg cccatgcccag cctccgctat aaccccccag 1250
aacgccagct ctatgcctgg gatgatggct accagattgt ctataagctg 1300
gagatgagga agaaagagga ggaggttga ggagctagcc ttgtttttg 1350
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ttcctcattc ttcaaatgtg ggccagttgt ggctcaa^{atc} ctctatattt 1450
ttagccaatg gcaatcaa atcttcagct cctttgttcc atacggact 1500
ccagatcctg agtaatcctt ttagagcccg aagagtcaaa accctcaatg 1550
ttccctcctg ctctcctgccc ccatgtcaac aaatttcagg ctaaggatgc 1600
cccagaccca gggctctaac cttgtatgcg ggcaggccca gggagcaggc 1650
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aacaggactt tctccacatt gttttgtatt gcaacattt gcattaaaag 1800
aaaaatccac aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1850

aaaaaaaaaaa aaaaaaaaaaa aaaaaaaaaaa aaa 1883

<210> 146

<211> 406

<212> PRT

<213> Homo sapiens

<400> 146

Met	Gly	Pro	Ser	Thr	Pro	Leu	Leu	Ile	Leu	Phe	Leu	Leu	Ser	Trp
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Ser	Gly	Pro	Leu	Gln	Gly	Gln	Gln	His	His	Leu	Val	Glu	Tyr	Met
				20					25					30
Glu	Arg	Arg	Leu	Ala	Ala	Leu	Glu	Glu	Arg	Leu	Ala	Gln	Cys	Gln
					35				40					45
Asp	Gln	Ser	Ser	Arg	His	Ala	Ala	Glu	Leu	Arg	Asp	Phe	Lys	Asn
					50				55					60
Lys	Met	Leu	Pro	Leu	Leu	Glu	Val	Ala	Glu	Lys	Glu	Arg	Glu	Ala
					65				70					75
Leu	Arg	Thr	Glu	Ala	Asp	Thr	Ile	Ser	Gly	Arg	Val	Asp	Arg	Leu
					80				85					90
Glu	Arg	Glu	Val	Asp	Tyr	Leu	Glu	Thr	Gln	Asn	Pro	Ala	Leu	Pro
					95				100					105
Cys	Val	Glu	Phe	Asp	Glu	Lys	Val	Thr	Gly	Gly	Pro	Gly	Thr	Lys
					110				115					120
Gly	Lys	Gly	Arg	Arg	Asn	Glu	Lys	Tyr	Asp	Met	Val	Thr	Asp	Cys
					125				130					135
Gly	Tyr	Thr	Ile	Ser	Gln	Val	Arg	Ser	Met	Lys	Ile	Leu	Lys	Arg
					140				145					150
Phe	Gly	Gly	Pro	Ala	Gly	Leu	Trp	Thr	Lys	Asp	Pro	Leu	Gly	Gln
					155				160					165
Thr	Glu	Lys	Ile	Tyr	Val	Leu	Asp	Gly	Thr	Gln	Asn	Asp	Thr	Ala
					170				175					180
Phe	Val	Phe	Pro	Arg	Leu	Arg	Asp	Phe	Thr	Leu	Ala	Met	Ala	Ala
					185				190					195
Arg	Lys	Ala	Ser	Arg	Val	Arg	Val	Pro	Phe	Pro	Trp	Val	Gly	Thr
					200				205					210
Gly	Gln	Leu	Val	Tyr	Gly	Gly	Phe	Leu	Tyr	Phe	Ala	Arg	Arg	Pro
					215				220					225
Pro	Gly	Arg	Pro	Gly	Gly	Gly	Glu	Met	Glu	Asn	Thr	Leu	Gln	
					230				235					240
Leu	Ile	Lys	Phe	His	Leu	Ala	Asn	Arg	Thr	Val	Val	Asp	Ser	Ser
					245				250					255

Val Phe Pro Ala Glu Gly Leu Ile Pro Pro Tyr Gly Leu Thr Ala
260 265 270
Asp Thr Tyr Ile Asp Leu Val Ala Asp Glu Glu Gly Leu Trp Ala
275 280 285
Val Tyr Ala Thr Arg Glu Asp Asp Arg His Leu Cys Leu Ala Lys
290 295 300
Leu Asp Pro Gln Thr Leu Asp Thr Glu Gln Gln Trp Asp Thr Pro
305 310 315
Cys Pro Arg Glu Asn Ala Glu Ala Ala Phe Val Ile Cys Gly Thr
320 325 330
Leu Tyr Val Val Tyr Asn Thr Arg Pro Ala Ser Arg Ala Arg Ile
335 340 345
Gln Cys Ser Phe Asp Ala Ser Gly Thr Leu Thr Pro Glu Arg Ala
350 355 360
Ala Leu Pro Tyr Phe Pro Arg Arg Tyr Gly Ala His Ala Ser Leu
365 370 375
Arg Tyr Asn Pro Arg Glu Arg Gln Leu Tyr Ala Trp Asp Asp Gly
380 385 390
Tyr Gln Ile Val Tyr Lys Leu Glu Met Arg Lys Lys Glu Glu Glu
395 400 405

Val

<210> 147
<211> 2052
<212> DNA
<213> Homo sapiens

<400> 147
gacagctgtg tctcgatgga gtagactctc agaacagcgc agtttgcct 50
ccgctcacgc agaggctctc cgtggcttcc gcacctttag cattaggcca 100
gttctccctct tctctcta at ccatccgtca cctctcctgt catccgttcc 150
catgccgtga ggtccattca cagaacacat ccatggctct catgctcagt 200
ttggttctga gtctcctcaa gctggatca gggcagtggc aggtgtttgg 250
gccagacaag cctgtccagg cttgggtgg ggaggacgca gcattctcct 300
gtttcctgtc tcctaagacc aatgcagagg ccatggaagt gcggttcttc 350
agggggccagt tctctagcgt ggtccacctc tacagggacg ggaaggacca 400
gccatattatg cagatgccac agtatcaagg caggacaaaa ctggtaagg 450
attctattgc ggaggggcgc atctctgtc ggctggaaaa cattactgt 500

ttggatgctg gcctctatgg gtgcaggatt agtcccagt cttaactacca 550
gaaggccatc tggagctac aggtgtcagc actgggctca gttcctctca 600
tttccatcac gggatatgtt gatagagaca tccagctact ctgtcagtcc 650
tcgggctgg tccccggcc cacagcgaag tggaaaggc cacaaggaca 700
ggatttgc acagactcca ggacaaacag' agacatgcat ggcctgttg 750
atgtggagat ctctctgacc gtccaagaga acgccggag catatcctgt 800
tccatgcggc atgctcatct gagccgagag gtggaatcca gggtacagat 850
aggagatacc ttttcgagc ctatatcgta gcacctggct accaaagtac 900
tggaataact ctgctgtggc ctattttg gcattgttg actgaagatt 950
ttcttccca aattccagtg gaaaatccag gcggactgg actggagaag 1000
aaagcacgga caggcagaat tgagagacgc ccggaaacac gcagtggagg 1050
tgactctgga tccagagacg gtcacccga agctctgcgt ttctgatctg 1100
aaaactgtaa cccatagaaa agctccccag gaggtgcctc actctgagaa 1150
gagatttaca aggaagagtg tggggcttc tcagagttc caagcaggg 1200
aacattactg ggaggtggac ggaggacaca ataaaaggta ggcgtggga 1250
gtgtgccggg atgatgtgga caggaggaag gagtacgtga ctttgcctcc 1300
cgatcatggg tactgggtcc tcagactgaa tggagaacat ttgtatttca 1350
cattaaatcc ccgttttac agcgtttcc ccaggacccc acctacaaaa 1400
ataggggtct tcctggacta tgagtgtggg accatctcct tcttcaacat 1450
aaatgaccag tcccttattt ataccctgac atgtcggtt gaaggcttat 1500
tgaggcccta cattgagttt ccgtcctata atgagcaaaa tggaaactccc 1550
atagtcatct gcccagtac ccaggaatca gagaaagagg cctttggca 1600
aaggccctct gcaatcccag agacaagcaa cagtggatcc tcctcacagg 1650
caaccacgcc cttccccc aggggtgaaa tgttaggatga atcacatccc 1700
acattcttct ttagggatat taaggctct ctccagatc caaagtcccc 1750
cagcagccgg ccaaggtggc ttccagatga agggggactg gcctgtccac 1800
atgggagtca ggtgtcatgg ctgcctgag ctggggaggga agaaggctga 1850
cattacattt agtttgcctct cactccatct ggcttaagtga tcttgaata 1900
ccacctctca ggtgaagaac cgtcaggaat tcccatctca caggctgtgg 1950

tgtagattaa gtagacaagg aatgtgaata atgcttagat cttattgatg 2000
acagagtgtt tcctaatggc ttgttcatta tattacactt tcagtaaaaa 2050
aa 2052

<210> 148
<211> 500
<212> PRT
<213> Homo sapiens

<400> 148

Met	Ala	Leu	Met	Leu	Ser	Leu	Val	Leu	Ser	Leu	Leu	Lys	Leu	Gly
1														15
Ser	Gly	Gln	Trp	Gln	Val	Phe	Gly	Pro	Asp	Lys	Pro	Val	Gln	Ala
					20				25					30
Leu	Val	Gly	Glu	Asp	Ala	Ala	Phe	Ser	Cys	Phe	Leu	Ser	Pro	Lys
					35				40					45
Thr	Asn	Ala	Glu	Ala	Met	Glu	Val	Arg	Phe	Phe	Arg	Gly	Gln	Phe
					50				55					60
Ser	Ser	Val	Val	His	Leu	Tyr	Arg	Asp	Gly	Lys	Asp	Gln	Pro	Phe
					65				70					75
Met	Gln	Met	Pro	Gln	Tyr	Gln	Gly	Arg	Thr	Lys	Leu	Val	Lys	Asp
					80				85					90
Ser	Ile	Ala	Glu	Gly	Arg	Ile	Ser	Leu	Arg	Leu	Glu	Asn	Ile	Thr
					95				100					105
Val	Leu	Asp	Ala	Gly	Leu	Tyr	Gly	Cys	Arg	Ile	Ser	Ser	Gln	Ser
					110				115					120
Tyr	Tyr	Gln	Lys	Ala	Ile	Trp	Glu	Leu	Gln	Val	Ser	Ala	Leu	Gly
					125				130					135
Ser	Val	Pro	Leu	Ile	Ser	Ile	Thr	Gly	Tyr	Val	Asp	Arg	Asp	Ile
					140				145					150
Gln	Leu	Leu	Cys	Gln	Ser	Ser	Gly	Trp	Phe	Pro	Arg	Pro	Thr	Ala
					155				160					165
Lys	Trp	Lys	Gly	Pro	Gln	Gly	Gln	Asp	Leu	Ser	Thr	Asp	Ser	Arg
					170				175					180
Thr	Asn	Arg	Asp	Met	His	Gly	Leu	Phe	Asp	Val	Glu	Ile	Ser	Leu
					185				190					195
Thr	Val	Gln	Glu	Asn	Ala	Gly	Ser	Ile	Ser	Cys	Ser	Met	Arg	His
					200				205					210
Ala	His	Leu	Ser	Arg	Glu	Val	Glu	Ser	Arg	Val	Gln	Ile	Gly	Asp
					215				220					225
Thr	Phe	Phe	Glu	Pro	Ile	Ser	Trp	His	Leu	Ala	Thr	Lys	Val	Leu

230	235	240
Gly Ile Leu Cys Cys Gly Leu Phe Phe	Gly Ile Val Gly Leu Lys	
245 250	255	
Ile Phe Phe Ser Lys Phe Gln Trp Lys	Ile Gln Ala Glu Leu Asp	
260 265	270	
Trp Arg Arg Lys His Gly Gln Ala Glu	Leu Arg Asp Ala Arg Lys	
275 280	285	
His Ala Val Glu Val Thr Leu Asp Pro	Glu Thr Ala His Pro Lys	
290 295	300	
Leu Cys Val Ser Asp Leu Lys Thr Val	Thr His Arg Lys Ala Pro	
305 310	315	
Gln Glu Val Pro His Ser Glu Lys Arg	Phe Thr Arg Lys Ser Val	
320 325	330	
Val Ala Ser Gln Ser Phe Gln Ala Gly	Lys His Tyr Trp Glu Val	
335 340	345	
Asp Gly Gly His Asn Lys Arg Trp Arg	Val Gly Val Cys Arg Asp	
350 355	360	
Asp Val Asp Arg Arg Lys Glu Tyr Val	Thr Leu Ser Pro Asp His	
365 370	375	
Gly Tyr Trp Val Leu Arg Leu Asn Gly	Glu His Leu Tyr Phe Thr	
380 385	390	
Leu Asn Pro Arg Phe Ile Ser Val Phe	Pro Arg Thr Pro Pro Thr	
395 400	405	
Lys Ile Gly Val Phe Leu Asp Tyr Glu	Cys Gly Thr Ile Ser Phe	
410 415	420	
Phe Asn Ile Asn Asp Gln Ser Leu Ile	Tyr Thr Leu Thr Cys Arg	
425 430	435	
Phe Glu Gly Leu Leu Arg Pro Tyr Ile	Glu Tyr Pro Ser Tyr Asn	
440 445	450	
Glu Gln Asn Gly Thr Pro Ile Val Ile	Cys Pro Val Thr Gln Glu	
455 460	465	
Ser Glu Lys Glu Ala Ser Trp Gln Arg	Ala Ser Ala Ile Pro Glu	
470 475	480	
Thr Ser Asn Ser Glu Ser Ser Ser Gln	Ala Thr Thr Pro Phe Leu	
485 490	495	
Pro Arg Gly Glu Met		
500		

<210> 149
<211> 24

<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 149
gctgttgtcca cctctacagg gacg 24

<210> 150
<211> 23
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-23
<223> Synthetic construct.

<400> 150
gaaactgacc cagtgtgac acc 23

<210> 151
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 151
gcagatgcca cagtatcaag gcaggacaaa actggtaag gattc 45

<210> 152
<211> 2294
<212> DNA
<213> Homo sapiens

<400> 152
gcgatggtgc gcccgggtggc ggtggcggcg gcgggtgcgg aggcttcctt 50
ggtcggattg caacgaggag aagatgactg accaaccgac tggctgaatg 100
aatgaatggc ggagccgagc gcgccatgag gagcctgccc agcctggcg 150
gcctcgccct gttgtgctgc gcccggcccg ccggccggcgt cgcctcagcc 200
gcctcggcgg ggaatgtcac cgggtggcggc gggccgcgg ggcagggtgga 250
cgcgtcgccg ggccccgggt tgcggggcga gcccagccac cccttcctta 300
gggcgacggc tcccacggcc caggccccga ggaccgggcc cccgcgcgcc 350
accgtccacc gaccctggc tgcgacttct ccagccccagt cccccggagac 400

caccctttt tggcgactg ctggaccctc ttccaccacc tttcaggcgc 450
cgctcgccc ctcggcacc acccctccgg cgccggaacg cacttcgacc 500
acctctcagg cgccgaccag acccgccgacc accaccctt cgacgaccac 550
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gccatgtgac tgttagtccac atggagctct cagcataccg tgcaacaggt 900
aagcaacaga gggtggact gaagtttatt ttattttagc aaggaaaaaa 950
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gggtcataga tttacaaaat attttatata cttttattct cttactttat 1050
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taccagtaca ttttgagac caaaagtaga ttaagcagga attatcttta 1450
aactattatg ttatggag gtaatthaat ctatggaaat aatgtactgt 1500
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tggaggttgc agtgagctga gatcgccca ctgcactcca gcctggtag 2250
agagggagac tctgtcttaa aaaaaaaaaa aaaaaaaaaa aaaa 2294

<210> 153

<211> 258

<212> PRT

<213> Homo sapiens

<400> 153

Met Arg Ser Leu Pro Ser Leu Gly Gly Leu Ala Leu Leu Cys Cys
1 5 10 15

Ala Ala Ala Ala Ala Ala Val Ala Ser Ala Ala Ser Ala Gly Asn
20 25 30

Val Thr Gly Gly Gly Ala Ala Gly Gln Val Asp Ala Ser Pro
35 40 45

Gly Pro Gly Leu Arg Gly Glu Pro Ser His Pro Phe Pro Arg Ala
50 55 60

Thr Ala Pro Thr Ala Gln Ala Pro Arg Thr Gly Pro Pro Arg Ala
65 70 75

Thr Val His Arg Pro Leu Ala Ala Thr Ser Pro Ala Gln Ser Pro
80 85 .. 90

Glu Thr Thr Pro Leu Trp Ala Thr Ala Gly Pro Ser Ser Thr Thr
95 100 105

Phe Gln Ala Pro Leu Gly Pro Ser Pro Thr Thr Pro Pro Ala Ala
110 115 120

Glu Arg Thr Ser Thr Ser Gln Ala Pro Thr Arg Pro Ala Pro
125 130 135

Thr Thr Leu Ser Thr Thr Gly Pro Ala Pro Thr Thr Pro Val
140 145 150

Ala Thr Thr Val Pro Ala Pro Thr Thr Pro Arg Thr Pro Thr Pro
155 160 165

Asp Leu Pro Ser Ser Ser Asn Ser Ser Val Leu Pro Thr Pro Pro

170	175	180
Ala Thr Glu Ala Pro Ser Ser Pro Pro Pro	Glu Tyr Val Cys Asn	
185	190	195
Cys Ser Val Val Gly Ser Leu Asn Val Asn Arg Cys Asn Gln Thr		
200	205	210
Thr Gly Gln Cys Glu Cys Arg Pro Gly Tyr Gln Gly Leu His Cys		
215	220	225
Glu Thr Cys Lys Glu Gly Phe Tyr Leu Asn Tyr Thr Ser Gly Leu		
230	235	240
Cys Gln Pro Cys Asp Cys Ser Pro His Gly Ala Leu Ser Ile Pro		
245	250	255
Cys Asn Arg		

<210> 154

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 154

aactgctctg tggttggaag cctg 24

<210> 155

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 155

cagtcacatg gctgacagac ccac 24

<210> 156

<211> 38

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-38

<223> Synthetic construct.

<400> 156

aggttatcag gggcttcact gtgaaacctg caaagagg 38

<210> 157
<211> 689
<212> DNA
<213> Homo sapiens

<400> 157
tgcggcgcag tgtagacctg ggaggatggg cggcctgctg ctggctgctt 50
ttctggctt ggtctcggtg cccagggccc aggccgtgtg gttggaaaga 100
ctggaccctg agcagcttct tggccctgg tacgtgcttgcggcctc 150
ccgggaaaag ggcttgcca tggagaagga catgaagaac gtcgtgggg 200
tggtggtgac cctcactcca gaaaacaacc tgcggacgct gtcctctcag 250
cacgggctgg gaggggtgtga ccagagtgtc atggacactga taaagcgaaa 300
ctccggatgg gtgttgaga atccctcaat aggctgtgtg gagctctggg 350
tgctggccac caacttcaga gactatgcca tcatcttcac tcagctggag 400
ttcggggacg agcccttcaa caccgtggag ctgtacagtc tgacggagac 450
agccagccag gaggccatgg ggctcttac caagtggagc aggagcctgg 500
gcttcctgtc acagtagcag gcccagctgc agaaggacct cacctgtgct 550
cacaagatcc ttctgtgagt gtcgtccc cagtagggat ggcgcccaca 600
gggtcctgtg acctcggcca gtgtccaccc acctcgctca gcggctcccg 650
gggcccagca ccagctcaga ataaagcgat tccacagca 689

<210> 158
<211> 163
<212> PRT
<213> Homo sapiens

<400> 158
Met Gly Gly Leu Leu Leu Ala Ala Phe Leu Ala Leu Val Ser Val
1 5 10 15
Pro Arg Ala Gln Ala Val Trp Leu Gly Arg Leu Asp Pro Glu Gln
20 25 30
Leu Leu Gly Pro Trp Tyr Val Leu Ala Val Ala Ser Arg Glu Lys
35 40 45
Gly Phe Ala Met Glu Lys Asp Met Lys Asn Val Val Gly Val Val
50 55 60
Val Thr Leu Thr Pro Glu Asn Asn Leu Arg Thr Leu Ser Ser Gln
65 70 75
His Gly Leu Gly Gly Cys Asp Gln Ser Val Met Asp Leu Ile Lys
80 85 90

Arg Asn Ser Gly Trp Val Phe Glu Asn Pro Ser Ile Gly Val Leu
95 100 105

Glu Leu Trp Val Leu Ala Thr Asn Phe Arg Asp Tyr Ala Ile Ile
110 115 120

Phe Thr Gln Leu Glu Phe Gly Asp Glu Pro Phe Asn Thr Val Glu
125 130 135

Leu Tyr Ser Leu Thr Glu Thr Ala Ser Gln Glu Ala Met Gly Leu
140 145 150

Phe Thr Lys Trp Ser Arg Ser Leu Gly Phe Leu Ser Gln
155 160

<210> 159

<211> 1665

<212> DNA

<213> Homo sapiens

<400> 159

aacagacgtt ccctcgccgc cctggcacct ctaacccag acatgctgct 50

gctgctgctg cccctgctct gggggaggga gagggcggaa ggacagacaa 100

gtaaaactgct gacgatgcag agttccgtga cggtgcagga aggccctgtgt 150

gtccatgtgc cctgctcctt ctcctacccc tcgcacggct ggatttaccc 200

tggcccagta gttcatggct actgggtccg ggaaggggcc aatacagacc 250

aggatgctcc agtgccaca aacaacccag ctcggcagt gtgggaggag 300

actcgggacc gattccacct ccttggggac ccacatacca agaattgcac 350

cctgagcatc agagatgcca gaagaagtga tgcggggaga tacttcttc 400

gtatggagaa aggaagtata aaatggaaatt ataaacatca ccggctctct 450

gtaatgtga cagccttgac ccacaggccc aacatcctca tcccaggcac 500

cctggagtcc ggctgcccc agaatctgac ctgctctgtc ccctgggcct 550

gtgagcaggg gacacccct atgatctcct ggatagggac ctccgtgtcc 600

ccccctggacc cctccaccac ccgctcctcg gtgctcaccc tcataccaca 650

gccccaggac catggcacca gcctcacctg tcaggtgacc ttccctgggg 700

ccagcgtgac cacgaacaag accgtccatc tcaacgtgtc ctacccgcct 750

cagaacttga ccatgactgt cttccaagga gacggcacag tatccacagt 800

cttgggaaat ggctcatctc tgtcaactccc agagggccag tctctgcgcc 850

tggctgtgc agttgatgca gttgacagca atccccctgc caggctgagc 900

ctgagctgga gaggcctgac cctgtgcccc tcacagccct caaacccggg 950

ggtgctggag ctgccttggg tgcacccctgag ggcgcagct gaattcacct 1000
gcagagctca gaaccctctc ggctctcagc aggtctaccc gaacgtctcc 1050
ctgcagagca aagccacatc aggagtgact caggggggtgg tcgggggagc 1100
tggagccaca gccctggtct tcctgtcctt ctgcgtcatc ttcgtttag 1150
tgaggtcctg caggaagaaa tcggcaaggc cagcagcggg cgtgggagat 1200
acgggcatacg aggatgcaaa cgctgtcagg ggttcagcct ctcaggggcc 1250
cctgactgaa ccttggcag aagacagtcc cccagaccag cctccccag 1300
cttctgcccgt ctcctcagtgg gggaaaggag agctccagta tgcataccctc 1350
agcttccaga tggtaagcc ttgggactcg cggggacagg aggccactga 1400
caccgagttac tcggagatca agatccacag atgagaaact gcagagactc 1450
accctgatttgggatcaca gcccctccag gcaagggaga agtcagagggc 1500
tgattcttgtt agaatttaca gcccctaactc tgatgagcta tgataacact 1550
atgaaattatgtt tgcagagtga aaagcacaca ggcttttagag tcaaagtatc 1600
tcaaacctga atccacactg tgccctccct tttttttttaactaaaag 1650
acagacaaat tccta 1665

<210> 160

<211> 463

<212> PRT

<213> Homo sapiens

<400> 160

Met	Leu	Leu	Leu	Leu	Leu	Pro	Leu	Leu	Trp	Gly	Arg	Glu	Arg	Ala
1					5				10					15
Glu	Gly	Gln	Thr	Ser	Lys	Leu	Leu	Thr	Met	Gln	Ser	Ser	Val	Thr
					20				25					30
Val	Gln	Glu	Gly	Leu	Cys	Val	His	Val	Pro	Cys	Ser	Phe	Ser	Tyr
				35				40						45
Pro	Ser	His	Gly	Trp	Ile	Tyr	Pro	Gly	Pro	Val	Val	His	Gly	Tyr
				50				55						60
Trp	Phe	Arg	Glu	Gly	Ala	Asn	Thr	Asp	Gln	Asp	Ala	Pro	Val	Ala
				65				70						75
Thr	Asn	Asn	Pro	Ala	Arg	Ala	Val	Trp	Glu	Glu	Thr	Arg	Asp	Arg
				80				85						90
Phe	His	Leu	Leu	Gly	Asp	Pro	His	Thr	Lys	Asn	Cys	Thr	Leu	Ser
				95				100						105
Ile	Arg	Asp	Ala	Arg	Arg	Ser	Asp	Ala	Gly	Arg	Tyr	Phe	Phe	Arg

110	115	120
Met Glu Lys Gly Ser Ile Lys Trp Asn Tyr Lys His His Arg Leu		
125	130	135
Ser Val Asn Val Thr Ala Leu Thr His Arg Pro Asn Ile Leu Ile		
140	145	150
Pro Gly Thr Leu Glu Ser Gly Cys Pro Gln Asn Leu Thr Cys Ser		
155	160	165
Val Pro Trp Ala Cys Glu Gln Gly Thr Pro Pro Met Ile Ser Trp		
170	175	180
Ile Gly Thr Ser Val Ser Pro Leu Asp Pro Ser Thr Thr Arg Ser		
185	190	195
Ser Val Leu Thr Leu Ile Pro Gln Pro Gln Asp His Gly Thr Ser		
200	205	210
Leu Thr Cys Gln Val Thr Phe Pro Gly Ala Ser Val Thr Thr Asn		
215	220	225
Lys Thr Val His Leu Asn Val Ser Tyr Pro Pro Gln Asn Leu Thr		
230	235	240
Met Thr Val Phe Gln Gly Asp Gly Thr Val Ser Thr Val Leu Gly		
245	250	255
Asn Gly Ser Ser Leu Ser Leu Pro Glu Gly Gln Ser Leu Arg Leu		
260	265	270
Val Cys Ala Val Asp Ala Val Asp Ser Asn Pro Pro Ala Arg Leu		
275	280	285
Ser Leu Ser Trp Arg Gly Leu Thr Leu Cys Pro Ser Gln Pro Ser		
290	295	300
Asn Pro Gly Val Leu Glu Leu Pro Trp Val His Leu Arg Asp Ala		
305	310	315
Ala Glu Phe Thr Cys Arg Ala Gln Asn Pro Leu Gly Ser Gln Gln		
320	325	330
Val Tyr Leu Asn Val Ser Leu Gln Ser Lys Ala Thr Ser Gly Val		
335	340	345
Thr Gln Gly Val Val Gly Gly Ala Gly Ala Thr Ala Leu Val Phe		
350	355	360
Leu Ser Phe Cys Val Ile Phe Val Val Val Arg Ser Cys Arg Lys		
365	370	375
Lys Ser Ala Arg Pro Ala Ala Gly Val Gly Asp Thr Gly Ile Glu		
380	385	390
Asp Ala Asn Ala Val Arg Gly Ser Ala Ser Gln Gly Pro Leu Thr		
395	400	405

Glu Pro Trp Ala Glu Asp Ser Pro Pro Asp Gln Pro Pro Pro Ala
410 415 420

Ser Ala Arg Ser Ser Val Gly Gly Glu Leu Gln Tyr Ala Ser
425 430 435

Leu Ser Phe Gln Met Val Lys Pro Trp Asp Ser Arg Gly Gln Glu
440 445 450

Ala Thr Asp Thr Glu Tyr Ser Glu Ile Lys Ile His Arg
455 460

<210> 161

<211> 739

<212> DNA

<213> Homo sapiens

<400> 161

gacgcccagt gacctgccga ggtcggcagc acagagctct ggagatgaag 50

accctgttcc tgggtgtcac gtcggcctg gccgctgccc tgtccttcac 100

cctggaggag gaggatatac cagggacctg gtacgtgaag gccatggtgg 150

tcgataagga ctttccggag gacaggaggc ccaggaaggt gtccccagtg 200

aaggtgacag ccctggcg 500

tgaaaatggtgaagccatgt tcaccttcat 250

gagggaggat cggtgcattcc agaagaaaat cctgatgcgg aagacggagg 300

agcctggcaa atacagcgcc tatggggca ggaagctcat gtacctgcag 350

gagctgccc 550

ggagggacca ctacatctt tactgcaaag accagcacca 400

tggggcctg ctccacatgg gaaagcttgt gggtaggaat tctgatacca 450

accgggaggc cctgaaagaa tttaagaaat tggtgcagcg caagggactc 500

tcggaggagg acattttcac gcccctgcag acggaaagct gcgttcccga 550

acactaggca gccccgggt ctgcaccc 600

agagccacc ctaccaccag

acacagagcc 650

cgaccaccc tccagccatg acccttcct

gctcccaccc acctgactcc aaataaagtc 700

aaaaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 739

<210> 162

<211> 170

<212> PRT

<213> Homo sapiens

<400> 162

Met Lys Thr Leu Phe Leu Gly Val Thr Leu Gly Leu Ala Ala Ala
1 5 10 15

Leu Ser Phe Thr Leu Glu Glu Asp Ile Thr Gly Thr Trp Tyr

20	25	30
Val Lys Ala Met Val Val Asp Lys Asp Phe Pro Glu Asp Arg Arg		
35	40	45
Pro Arg Lys Val Ser Pro Val Lys Val Thr Ala Leu Gly Gly Gly		
50	55	60
Lys Leu Glu Ala Thr Phe Thr Phe Met Arg Glu Asp Arg Cys Ile		
65	70	75
Gln Lys Lys Ile Leu Met Arg Lys Thr Glu Glu Pro Gly Lys Tyr		
80	85	90
Ser Ala Tyr Gly Gly Arg Lys Leu Met Tyr Leu Gln Glu Leu Pro		
95	100	105
Arg Arg Asp His Tyr Ile Phe Tyr Cys Lys Asp Gln His His Gly		
110	115	120
Gly Leu Leu His Met Gly Lys Leu Val Gly Arg Asn Ser Asp Thr		
125	130	135
Asn Arg Glu Ala Leu Glu Glu Phe Lys Lys Leu Val Gln Arg Lys		
140	145	150
Gly Leu Ser Glu Glu Asp Ile Phe Thr Pro Leu Gln Thr Gly Ser		
155	160	165
Cys Val Pro Glu His		
170		

<210> 163
<211> 22
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-22
<223> Synthetic construct.

<400> 163
ggagatgaag accctgttcc tg 22

<210> 164
<211> 26
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-26
<223> Synthetic construct.

<400> 164
ggagatgaag accctgttcc tgggtg 26

<210> 165
<211> 21
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-21
<223> Synthetic construct.

<400> 165
gtcctccgga aagtccatat c 21

<210> 166
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-25
<223> Synthetic construct.

<400> 166
gccttagtgtt cggaaacgca gcttc 25

<210> 167
<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 167
caggcacctg gtacgtgaag gccatggtgg tcgataagga ctttccggag 50

<210> 168
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 168
ctgtccttca ccctggagga ggaggatatac acagggaccc ggtac 45

<210> 169
<211> 1204
<212> DNA
<213> Homo sapiens

<400> 169

gttccgcaga tgcagagggtt gaggtggctg cgggactgga agtcatcggg 50
cagaggtctc acagcagcca aggaacctgg ggcccgctcc tccccctcc 100
aggccatgag gattctgcag ttaatcctgc ttgctctggc aacagggctt 150
gtagggggag agaccaggat catcaagggg ttcgagtgc agcctcaactc 200
ccagccctgg caggcagccc tggcgagaa gacgcggcta ctctgtgggg 250
cgacgctcat cgcccccaaga tggctcctga cagcagccca ctgcctcaag 300
ccccgctaca tagttcacct ggggcagcac aacctccaga aggaggaggg 350
ctgtgagcag acccggacag ccactgagtc cttcccccac cccggcttca 400
acaacagcct ccccaacaaa gaccaccgca atgacatcat gctggtgaag 450
atggcatcgc cagtctccat cacctggct gtgcgacccc tcaccctctc 500
ctcacgctgt gtcactgctg gcaccagctg cctcatttcc ggctggggca 550
gcacgtccag cccccagttt cgcctgcctc acacccttgcg atgcgccaac 600
atcaccatca ttgagcacca gaagtgtgag aacgcctacc ccggcaacat 650
cacagacacc atggtgtgtg ccagcgtgca ggaaggggc aaggactcct 700
gccagggta ctccggggc cctctggct gtaaccagtc tcttcaaggc 750
attatctcct gggccagga tccgtgtgcg atcacccgaa agcctggtgt 800
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acaatttagac tggacccacc caccacagcc catcaccctc catttccact 900
tggtgtttgg ttccctgttca ctctgttaat aagaaaccct aagccaagac 950
cctctacgaa cattcttgg gcctccttgg ctacaggaga tgctgtcact 1000
taataatcaa cctggggttc gaaatcagtg agacctggat tcaaattctg 1050
ccttggaaata ttgtgactct gggaatgaca acacctgggt tttctctgt 1100
tgtatccccca gccccaaaga cagctcctgg ccatatatca aggtttcaat 1150
aaatatttgc taaatgaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1200
aaaa 1204

<210> 170
<211> 250
<212> PRT
<213> Homo sapiens

<400> 170
Met Arg Ile Leu Gln Leu Ile Leu Leu Ala Leu Ala Thr Gly Leu
1 5 10 15

Val	Gly	Gly	Glu	Thr	Arg	Ile	Ile	Lys	Gly	Phe	Glu	Cys	Lys	Pro
20														30
His	Ser	Gln	Pro	Trp	Gln	Ala	Ala	Leu	Phe	Glu	Lys	Thr	Arg	Leu
35														45
Leu	Cys	Gly	Ala	Thr	Leu	Ile	Ala	Pro	Arg	Trp	Leu	Leu	Thr	Ala
50														60
Ala	His	Cys	Leu	Lys	Pro	Arg	Tyr	Ile	Val	His	Leu	Gly	Gln	His
65														75
Asn	Leu	Gln	Lys	Glu	Glu	Gly	Cys	Glu	Gln	Thr	Arg	Thr	Ala	Thr
80														90
Glu	Ser	Phe	Pro	His	Pro	Gly	Phe	Asn	Asn	Ser	Leu	Pro	Asn	Lys
95														105
Asp	His	Arg	Asn	Asp	Ile	Met	Leu	Val	Lys	Met	Ala	Ser	Pro	Val
110														120
Ser	Ile	Thr	Trp	Ala	Val	Arg	Pro	Leu	Thr	Leu	Ser	Ser	Arg	Cys
125														135
Val	Thr	Ala	Gly	Thr	Ser	Cys	Leu	Ile	Ser	Gly	Trp	Gly	Ser	Thr
140														150
Ser	Ser	Pro	Gln	Leu	Arg	Leu	Pro	His	Thr	Leu	Arg	Cys	Ala	Asn
155														165
Ile	Thr	Ile	Ile	Glu	His	Gln	Lys	Cys	Glu	Asn	Ala	Tyr	Pro	Gly
170														180
Asn	Ile	Thr	Asp	Thr	Met	Val	Cys	Ala	Ser	Val	Gln	Glu	Gly	Gly
185														195
Lys	Asp	Ser	Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Asn
200														210
Gln	Ser	Leu	Gln	Gly	Ile	Ile	Ser	Trp	Gly	Gln	Asp	Pro	Cys	Ala
215														225
Ile	Thr	Arg	Lys	Pro	Gly	Val	Tyr	Thr	Lys	Val	Cys	Lys	Tyr	Val
230														240
Asp	Trp	Ile	Gln	Glu	Thr	Met	Lys	Asn						
245														250

<210> 171

<211> 25

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-25

<223> Synthetic construct.

<400> 171
ggctgcggga ctggaaagtca tcggg 25

<210> 172
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 172
ctccaggcca tgaggattct gcag 24

<210> 173
<211> 18
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 173
cctctggtct gtaaccag 18

<210> 174
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 174
tctgtgatgt tgccgggta ggcg 24

<210> 175
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-25
<223> Synthetic construct.

<400> 175
cgtgttagaca ccaggcttc gggtg 25

<210> 176
<211> 18
<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-18

<223> Synthetic construct.

<400> 176
cccttgatga tcctggtc 18

<210> 177

<211> 50

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-50

<223> Synthetic construct.

<400> 177
aggccatgag gattctgcag ttaatcctgc ttgctctggc aacagggtt 50

<210> 178

<211> 43

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-43

<223> Synthetic construct.

<400> 178
gagagaccag gatcatcaag gggttcgagt gcaagcctca ctc 43

<210> 179

<211> 907

<212> DNA

<213> Homo sapiens

<400> 179
gagcagtgtt ctgctggagc cgatgccaaa aaccatgcat ttcttattca 50
gattcattgt tttctttat ctgtggggcc ttttactgc tcagagacaa 100
aagaaagagg agagcaccga agaagtgaaa atagaagttt tgcatcgcc 150
agaaaaactgc tctaagacaa gcaagaaggg agacctacta aatgcccatt 200
atgacggctta cctggctaaa gacggctcga aattctactg cagccggaca 250
caaaaatgaag gccaccccaa atggtttgg tttgggtttg ggcaagtcat 300
aaaaggccta gacattgctta tgacagatat gtgcctgga gaaaagcgaa 350
aagtagttat acccccttca tttgcatacg gaaaggaagg ctatgcagaa 400

ggcaagattc caccggatgc tacattgatt tttgagattt aactttatgc 450
tgtgaccaaa ggaccacgga gcattgagac atttaaacaat atagacatgg 500
acaatgacag gcagctctct aaagccgaga taaacctcta cttgcaaagg 550
gaatttggaaa aagatgagaa gccacgtgac aagtcatatc aggatgcagt 600
tttagaagat attttaaga agaatgacca tgatggtgat ggcttcattt 650
ctcccaagga atacaatgta taccaacacg atgaactata gcattttgt 700
atttctactt tttttttta gctatttact gtactttatg tataaaaca 750
agtcactttt ctccaagttt tatttgctat ttttccctta tgagaagata 800
ttttgatctc cccaatacat tgatttttgtt ataataaatg tgaggctgtt 850
ttgcaaactt aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 900
aaaaaaaa 907

<210> 180

<211> 222

<212> PRT

<213> Homo sapiens

<400> 180

Met Pro Lys Thr Met His Phe Leu Phe Arg Phe Ile Val Phe Phe
1 5 10 15

Tyr Leu Trp Gly Leu Phe Thr Ala Gln Arg Gln Lys Lys Glu Glu
20 25 30

Ser Thr Glu Glu Val Lys Ile Glu Val Leu His Arg Pro Glu Asn
35 40 45

Cys Ser Lys Thr Ser Lys Lys Gly Asp Leu Leu Asn Ala His Tyr
50 55 60

Asp Gly Tyr Leu Ala Lys Asp Gly Ser Lys Phe Tyr Cys Ser Arg
65 70 75

Thr Gln Asn Glu Gly His Pro Lys Trp Phe Val Leu Gly Val Gly
80 85 90

Gln Val Ile Lys Gly Leu Asp Ile Ala Met Thr Asp Met Cys Pro
95 100 105

Gly Glu Lys Arg Lys Val Val Ile Pro Pro Ser Phe Ala Tyr Gly
110 115 120

Lys Glu Gly Tyr Ala Glu Gly Lys Ile Pro Pro Asp Ala Thr Leu
125 130 135

Ile Phe Glu Ile Glu Leu Tyr Ala Val Thr Lys Gly Pro Arg Ser
140 145 150

Ile Glu Thr Phe Lys Gln Ile Asp Met Asp Asn Asp Arg Gln Leu
155 160 165

Ser Lys Ala Glu Ile Asn Leu Tyr Leu Gln Arg Glu Phe Glu Lys
170 175 180

Asp Glu Lys Pro Arg Asp Lys Ser Tyr Gln Asp Ala Val Leu Glu
185 190 195

Asp Ile Phe Lys Lys Asn Asp His Asp Gly Asp Gly Phe Ile Ser
200 205 210

Pro Lys Glu Tyr Asn Val Tyr Gln His Asp Glu Leu
215 220

<210> 181
<211> 22
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-22
<223> Synthetic construct.

<400> 181
gtgttctgct ggagccgatg cc 22

<210> 182
<211> 18
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 182
gacatggaca atgacagg 18

<210> 183
<211> 18
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 183
cctttcagga tgttaggag 18

<210> 184
<211> 18
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 184
gatgtctgcc accccaag 18

<210> 185
<211> 27
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-27
<223> Synthetic construct.

<400> 185
gcatcctgat atgacttgtc acgtggc 27

<210> 186
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 186
tacaagaggg aagaggagtt gcac 24

<210> 187
<211> 52
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-52
<223> Synthetic construct.

<400> 187
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cc 52

<210> 188
<211> 573
<212> DNA
<213> Homo sapiens

<400> 188
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cccaaatgct tcctgtgtca ataacactca ctgcacctgc aaccatggat 150
atacttctgg atctggcag aaactattca cattccctt ggagacatgt 200
aacgccaggc atggggctc gcgcctgtaa tcccagttct ttgggaagcc 250
aaggcaggtg gatcacctga ggtcaggagt ttgagaccag cctggccaac 300
atagtgaaac cccgtgtcta ctaaaaatac aaaaatcagc cgggcgtggt 350
ggtgcattgc tgcaatccca gttactcggtt aggctgagggc aggagaatcg 400
cttgaactca ggaggcagaa gttgcagtga acccagatcc tgccattgca 450
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ccaaataaaag tacttatatt ctc 573

<210> 189

<211> 74

<212> PRT

<213> Homo sapiens

<400> 189

Met Gln Gly Pro Leu Leu Leu Pro Gly Leu Cys Phe Leu Leu Ser
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Leu Phe Gly Ala Val Thr Gln Lys Thr Lys Thr Ser Cys Ala Lys
20 25 30

Cys Pro Pro Asn Ala Ser Cys Val Asn Asn Thr His Cys Thr Cys
35 40 45

Asn His Gly Tyr Thr Ser Gly Ser Gly Gln Lys Leu Phe Thr Phe
50 55 60

Pro Leu Glu Thr Cys Asn Ala Arg His Gly Gly Ser Arg Leu
65 70

<210> 190

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 190

agggaccatt gcttcttcca ggcc 24

<210> 191

<211> 24

<212> DNA

<213> Artificial

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<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 191
cgttacatgt ctccaagggg aatg 24

<210> 192
<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 192
cctgtgctaa gtgccccca aatgcttcct gtgtcaataa cactcactgc 50

<210> 193
<211> 1091
<212> DNA
<213> Homo sapiens

<400> 193
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gactttggaa gtgaccacc atggggctca gcatctttt gctcctgtgt 150
gttcttggc tcagccaggc agccacacccg aagattttca atggcactga 200
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cagccagctc gactggaccg agcagatccg gcacagcggc ttctctgtga 400
cccatcccg ctacctggga gcctcgacga gccacgagca cgacctccgg 450
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caaggtctgg tgcctgggg gtctgtggg ccctgtggac aagatggcat 800

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ccctagctcc actcttggtg gcctggaaac ttcttggaaac tttaactcct 1000
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<210> 194
<211> 248
<212> PRT
<213> Homo sapiens

<400> 194

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Gln	Ala	Ala	Thr	Pro	Lys	Ile	Phe	Asn	Gly	Thr	Glu	Cys	Gly	Arg
					20				25					30
Asn	Ser	Gln	Pro	Trp	Gln	Val	Gly	Leu	Phe	Glu	Gly	Thr	Ser	Leu
					35				40					45
Arg	Cys	Gly	Gly	Val	Leu	Ile	Asp	His	Arg	Trp	Val	Leu	Thr	Ala
				50				55						60
Ala	His	Cys	Ser	Gly	Ser	Arg	Tyr	Trp	Val	Arg	Leu	Gly	Glu	His
				65				70						75
Ser	Leu	Ser	Gln	Leu	Asp	Trp	Thr	Glu	Gln	Ile	Arg	His	Ser	Gly
				80				85						90
Phe	Ser	Val	Thr	His	Pro	Gly	Tyr	Leu	Gly	Ala	Ser	Thr	Ser	His
				95				100						105
Glu	His	Asp	Leu	Arg	Leu	Leu	Arg	Leu	Arg	Leu	Pro	Val	Arg	Val
				110				115						120
Thr	Ser	Ser	Val	Gln	Pro	Leu	Pro	Leu	Pro	Asn	Asp	Cys	Ala	Thr
				125				130						135
Ala	Gly	Thr	Glu	Cys	His	Val	Ser	Gly	Trp	Gly	Ile	Thr	Asn	His
				140				145						150
Pro	Arg	Asn	Pro	Phe	Pro	Asp	Leu	Leu	Gln	Cys	Leu	Asn	Leu	Ser
				155				160						165
Ile	Val	Ser	His	Ala	Thr	Cys	His	Gly	Val	Tyr	Pro	Gly	Arg	Ile
				170				175						180
Thr	Ser	Asn	Met	Val	Cys	Ala	Gly	Gly	Val	Pro	Gly	Gln	Asp	Ala
				185				190						195
Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Gly	Gly	Val	Leu

200	205	210												
Gln	Gly	Leu	Val	Ser	Trp	Gly	Ser	Val	Gly	Pro	Cys	Gly	Gln	Asp
215								220					225	
Gly	Ile	Pro	Gly	Val	Tyr	Thr	Tyr	Ile	Cys	Lys	Tyr	Val	Asp	Trp
230								235					240	
Ile	Arg	Met	Ile	Met	Arg	Asn	Asn							
245														

<210> 195
<211> 1485
<212> DNA
<213> Homo sapiens

<400> 195
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tcgcccattgtc gggcgagctc agcaacaggt tccaaaggagg gaaggcggttc 150
ggcttgctca aagccggca ggagaggagg ctggccgaga tcaaccggga 200
gtttctgtgt gaccagaagt acagtgtatga agagaacctt ccagaaaagc 250
tcacagcctt caaagagaag tacatggagt ttgacacctgaa caatgaaggc 300
gagattgacc ttagtgtcttt aaagaggatg atggagaagc ttgggtgtccc 350
caagaccac ctggagatga agaagatgtat ctcagaggtg acaggagggg 400
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cggtcggtcg tcctcaagtt agtcatgtat tttgaaggaa aagccaacgaa 500
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<210> 196

<211> 150

<212> PRT

<213> Homo sapiens

<400> 196

Met Ser Gly Glu Leu Ser Asn Arg Phe Gln Gly Gly Lys Ala Phe
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Gly Leu Leu Lys Ala Arg Gln Glu Arg Arg Leu Ala Glu Ile Asn
20 25 30

Arg Glu Phe Leu Cys Asp Gln Lys Tyr Ser Asp Glu Glu Asn Leu
35 40 45

Pro Glu Lys Leu Thr Ala Phe Lys Glu Lys Tyr Met Glu Phe Asp
50 55 60

Leu Asn Asn Glu Gly Glu Ile Asp Leu Met Ser Leu Lys Arg Met
65 70 75

Met Glu Lys Leu Gly Val Pro Lys Thr His Leu Glu Met Lys Lys
80 85 90

Met Ile Ser Glu Val Thr Gly Gly Val Ser Asp Thr Ile Ser Tyr
95 100 105

Arg Asp Phe Val Asn Met Met Leu Gly Lys Arg Ser Ala Val Leu
110 115 120

Lys Leu Val Met Met Phe Glu Gly Lys Ala Asn Glu Ser Ser Pro
125 130 135

Lys Pro Val Gly Pro Pro Pro Glu Arg Asp Ile Ala Ser Leu Pro
140 145 150

<210> 197

<211> 4842

<212> DNA

<213> Homo sapiens

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<210> 198

<211> 1523

<212> PRT

<213> Homo sapiens

<400> 198

Met Ala Pro Gly Trp Ala Gly Val Gly Ala Ala Val Arg Ala Arg
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Leu Ala Leu Ala Leu Ala Leu Ala Ser Val Leu Ser Gly Pro Pro
20 25 30

Ala Val Ala Cys Pro Thr Lys Cys Thr Cys Ser Ala Ala Ser Val
35 40 45

Asp Cys His Gly Leu Gly Leu Arg Ala Val Pro Arg Gly Ile Pro
50 55 60

Arg Asn Ala Glu Arg Leu Asp Leu Asp Arg Asn Asn Ile Thr Arg
65 70 75

Ile Thr Lys Met Asp Phe Ala Gly Leu Lys Asn Leu Arg Val Leu
80 85 90

His Leu Glu Asp Asn Gln Val Ser Val Ile Glu Arg Gly Ala Phe
95 100 105

Gln Asp Leu Lys Gln Leu Glu Arg Leu Arg Leu Asn Lys Asn Lys
110 115 120

Leu Gln Val Leu Pro Glu Leu Leu Phe Gln Ser Thr Pro Lys Leu
125 130 135

Thr Arg Leu Asp Leu Ser Glu Asn Gln Ile Gln Gly Ile Pro Arg
140 145 150

Lys Ala Phe Arg Gly Ile Thr Asp Val Lys Asn Leu Gln Leu Asp
155 160 165

Asn Asn His Ile Ser Cys Ile Glu Asp Gly Ala Phe Arg Ala Leu
 170 175 180
 Arg Asp Leu Glu Ile Leu Thr Leu Asn Asn Asn Asn Ile Ser Arg
 185 190 195
 Ile Leu Val Thr Ser Phe Asn His Met Pro Lys Ile Arg Thr Leu
 200 205 210
 Arg Leu His Ser Asn His Leu Tyr Cys Asp Cys His Leu Ala Trp
 215 220 225
 Leu Ser Asp Trp Leu Arg Gln Arg Arg Thr Val Gly Gln Phe Thr
 230 235 240
 Leu Cys Met Ala Pro Val His Leu Arg Gly Phe Asn Val Ala Asp
 245 250 255
 Val Gln Lys Lys Glu Tyr Val Cys Pro Ala Pro His Ser Glu Pro
 260 265 270
 Pro Ser Cys Asn Ala Asn Ser Ile Ser Cys Pro Ser Pro Cys Thr
 275 280 285
 Cys Ser Asn Asn Ile Val Asp Cys Arg Gly Lys Gly Leu Met Glu
 290 295 300
 Ile Pro Ala Asn Leu Pro Glu Gly Ile Val Glu Ile Arg Leu Glu
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 Gln Asn Ser Ile Lys Ala Ile Pro Ala Gly Ala Phe Thr Gln Tyr
 320 325 330
 Lys Lys Leu Lys Arg Ile Asp Ile Ser Lys Asn Gln Ile Ser Asp
 335 340 345
 Ile Ala Pro Asp Ala Phe Gln Gly Leu Lys Ser Leu Thr Ser Leu
 350 355 360
 Val Leu Tyr Gly Asn Lys Ile Thr Glu Ile Ala Lys Gly Leu Phe
 365 370 375
 Asp Gly Leu Val Ser Leu Gln Leu Leu Leu Leu Asn Ala Asn Lys
 380 385 390
 Ile Asn Cys Leu Arg Val Asn Thr Phe Gln Asp Leu Gln Asn Leu
 395 400 405
 Asn Leu Leu Ser Leu Tyr Asp Asn Lys Leu Gln Thr Ile Ser Lys
 410 415 420
 Gly Leu Phe Ala Pro Leu Gln Ser Ile Gln Thr Leu His Leu Ala
 425 430 435
 Gln Asn Pro Phe Val Cys Asp Cys His Leu Lys Trp Leu Ala Asp
 440 445 450
 Tyr Leu Gln Asp Asn Pro Ile Glu Thr Ser Gly Ala Arg Cys Ser

455	460	465
Ser Pro Arg Arg Leu Ala Asn Lys Arg	Ile Ser Gln Ile Lys Ser	
470	475	480
Lys Lys Phe Arg Cys Ser Gly Ser Glu Asp	Tyr Arg Ser Arg Phe	
485	490	495
Ser Ser Glu Cys Phe Met Asp Leu Val	Cys Pro Glu Lys Cys Arg	
500	505	510
Cys Glu Gly Thr Ile Val Asp Cys Ser Asn	Gln Lys Leu Val Arg	
515	520	525
Ile Pro Ser His Leu Pro Glu Tyr Val	Thr Asp Leu Arg Leu Asn	
530	535	540
Asp Asn Glu Val Ser Val Leu Glu Ala	Thr Gly Ile Phe Lys Lys	
545	550	555
Leu Pro Asn Leu Arg Lys Ile Asn Leu	Ser Asn Asn Lys Ile Lys	
560	565	570
Glu Val Arg Glu Gly Ala Phe Asp Gly	Ala Ala Ser Val Gln Glu	
575	580	585
Leu Met Leu Thr Gly Asn Gln Leu Glu	Thr Val His Gly Arg Val	
590	595	600
Phe Arg Gly Leu Ser Gly Leu Lys Thr	Leu Met Leu Arg Ser Asn	
605	610	615
Leu Ile Ser Cys Val Ser Asn Asp Thr	Phe Ala Gly Leu Ser Ser	
620	625	630
Val Arg Leu Leu Ser Leu Tyr Asp Asn	Arg Ile Thr Thr Ile Thr	
635	640	645
Pro Gly Ala Phe Thr Thr Leu Val Ser	Leu Ser Thr Ile Asn Leu	
650	655	660
Leu Ser Asn Pro Phe Asn Cys Asn Cys	His Leu Ala Trp Leu Gly	
665	670	675
Lys Trp Leu Arg Lys Arg Arg Ile Val	Ser Gly Asn Pro Arg Cys	
680	685	690
Gln Lys Pro Phe Phe Leu Lys Glu Ile	Pro Ile Gln Asp Val Ala	
695	700	705
Ile Gln Asp Phe Thr Cys Asp Gly Asn	Glu Glu Ser Ser Cys Gln	
710	715	720
Leu Ser Pro Arg Cys Pro Glu Gln Cys	Thr Cys Met Glu Thr Val	
725	730	735
Val Arg Cys Ser Asn Lys Gly Leu Arg	Ala Leu Pro Arg Gly Met	
740	745	750

Pro Lys Asp Val Thr Glu Leu Tyr Leu Glu Gly Asn His Leu Thr
 755 760 765
 Ala Val Pro Arg Glu Leu Ser Ala Leu Arg His Leu Thr Leu Ile
 770 775 780
 Asp Leu Ser Asn Asn Ser Ile Ser Met Leu Thr Asn Tyr Thr Phe
 785 790 795
 Ser Asn Met Ser His Leu Ser Thr Leu Ile Leu Ser Tyr Asn Arg
 800 805 810
 Leu Arg Cys Ile Pro Val His Ala Phe Asn Gly Leu Arg Ser Leu
 815 820 825
 Arg Val Leu Thr Leu His Gly Asn Asp Ile Ser Ser Val Pro Glu
 830 835 840
 Gly Ser Phe Asn Asp Leu Thr Ser Leu Ser His Leu Ala Leu Gly
 845 850 855
 Thr Asn Pro Leu His Cys Asp Cys Ser Leu Arg Trp Leu Ser Glu
 860 865 870
 Trp Val Lys Ala Gly Tyr Lys Glu Pro Gly Ile Ala Arg Cys Ser
 875 880 885
 Ser Pro Glu Pro Met Ala Asp Arg Leu Leu Leu Thr Thr Pro Thr
 890 895 900
 His Arg Phe Gln Cys Lys Gly Pro Val Asp Ile Asn Ile Val Ala
 905 910 915
 Lys Cys Asn Ala Cys Leu Ser Ser Pro Cys Lys Asn Asn Gly Thr
 920 925 930
 Cys Thr Gln Asp Pro Val Glu Leu Tyr Arg Cys Ala Cys Pro Tyr
 935 940 945
 Ser Tyr Lys Gly Lys Asp Cys Thr Val Pro Ile Asn Thr Cys Ile
 950 955 960
 Gln Asn Pro Cys Gln His Gly Gly Thr Cys His Leu Ser Asp Ser
 965 970 975
 His Lys Asp Gly Phe Ser Cys Ser Cys Pro Leu Gly Phe Glu Gly
 980 985 990
 Gln Arg Cys Glu Ile Asn Pro Asp Asp Cys Glu Asp Asn Asp Cys
 995 1000 1005
 Glu Asn Asn Ala Thr Cys Val Asp Gly Ile Asn Asn Tyr Val Cys
 1010 1015 1020
 Ile Cys Pro Pro Asn Tyr Thr Gly Glu Leu Cys Asp Glu Val Ile
 1025 1030 1035
 Asp His Cys Val Pro Glu Leu Asn Leu Cys Gln His Glu Ala Lys

1040	1045	1050
Cys Ile Pro Leu Asp Lys Gly Phe Ser Cys Glu Cys Val Pro Gly		
1055	1060	1065
Tyr Ser Gly Lys Leu Cys Glu Thr Asp Asn Asp Asp Cys Val Ala		
1070	1075	1080
His Lys Cys Arg His Gly Ala Gln Cys Val Asp Thr Ile Asn Gly		
1085	1090	1095
Tyr Thr Cys Thr Cys Pro Gln Gly Phe Ser Gly Pro Phe Cys Glu		
1100	1105	1110
His Pro Pro Pro Met Val Leu Leu Gln Thr Ser Pro Cys Asp Gln		
1115	1120	1125
Tyr Glu Cys Gln Asn Gly Ala Gln Cys Ile Val Val Gln Gln Glu		
1130	1135	1140
Pro Thr Cys Arg Cys Pro Pro Gly Phe Ala Gly Pro Arg Cys Glu		
1145	1150	1155
Lys Leu Ile Thr Val Asn Phe Val Gly Lys Asp Ser Tyr Val Glu		
1160	1165	1170
Leu Ala Ser Ala Lys Val Arg Pro Gln Ala Asn Ile Ser Leu Gln		
1175	1180	1185
Val Ala Thr Asp Lys Asp Asn Gly Ile Leu Leu Tyr Lys Gly Asp		
1190	1195	1200
Asn Asp Pro Leu Ala Leu Glu Leu Tyr Gln Gly His Val Arg Leu		
1205	1210	1215
Val Tyr Asp Ser Leu Ser Ser Pro Pro Thr Thr Val Tyr Ser Val		
1220	1225	1230
Glu Thr Val Asn Asp Gly Gln Phe His Ser Val Glu Leu Val Thr		
1235	1240	1245
Leu Asn Gln Thr Leu Asn Leu Val Val Asp Lys Gly Thr Pro Lys		
1250	1255	1260
Ser Leu Gly Lys Leu Gln Lys Gln Pro Ala Val Gly Ile Asn Ser		
1265	1270	1275
Pro Leu Tyr Leu Gly Gly Ile Pro Thr Ser Thr Gly Leu Ser Ala		
1280	1285	1290
Leu Arg Gln Gly Thr Asp Arg Pro Leu Gly Gly Phe His Gly Cys		
1295	1300	1305
Ile His Glu Val Arg Ile Asn Asn Glu Leu Gln Asp Phe Lys Ala		
1310	1315	1320
Leu Pro Pro Gln Ser Leu Gly Val Ser Pro Gly Cys Lys Ser Cys		
1325	1330	1335

Thr Val Cys Lys His Gly Leu Cys Arg Ser Val Glu Lys Asp Ser
1340 1345 1350

Val Val Cys Glu Cys Arg Pro Gly Trp Thr Gly Pro Leu Cys Asp
1355 1360 1365

Gln Glu Ala Arg Asp Pro Cys Leu Gly His Arg Cys His His Gly
1370 1375 1380

Lys Cys Val Ala Thr Gly Thr Ser Tyr Met Cys Lys Cys Ala Glu
1385 1390 1395

Gly Tyr Gly Gly Asp Leu Cys Asp Asn Lys Asn Asp Ser Ala Asn
1400 1405 1410

Ala Cys Ser Ala Phe Lys Cys His His Gly Gln Cys His Ile Ser
1415 1420 1425

Asp Gln Gly Glu Pro Tyr Cys Leu Cys Gln Pro Gly Phe Ser Gly
1430 1435 1440

Glu His Cys Gln Gln Glu Asn Pro Cys Leu Gly Gln Val Val Arg
1445 1450 1455

Glu Val Ile Arg Arg Gln Lys Gly Tyr Ala Ser Cys Ala Thr Ala
1460 1465 1470

Ser Lys Val Pro Ile Met Glu Cys Arg Gly Gly Cys Gly Pro Gln
1475 1480 1485

Cys Cys Gln Pro Thr Arg Ser Lys Arg Arg Lys Tyr Val Phe Gln
1490 1495 1500

Cys Thr Asp Gly Ser Ser Phe Val Glu Glu Val Glu Arg His Leu
1505 1510 1515

Glu Cys Gly Cys Leu Ala Cys Ser
1520

<210> 199
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 199
atggagattc ctgccaactt gccg 24

<210> 200
<211> 24
<212> DNA
<213> Artificial

<220>

<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 200
ttgttggcat tgaggaggag cagc 24

<210> 201
<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 201
gagggcatcg tcgaaatacg cctagaacag aactccatca aagccatccc 50

<210> 202
<211> 753
<212> DNA
<213> Homo sapiens

<400> 202
ggatgcagga cgctccctg agctgcctgt caccgactag gtggagcagt 50
gtttcttccg cagactcaac tgagaagtca gcctctgggg caggcaccag 100
gaatctgcct tttcagttct gtctccggca ggcttgagg atgaaggctg 150
cgggcattct gaccctcatt ggctgcctgg tcacaggcgc cgagtccaaa 200
atctacactc gttgcaaact ggcaaaaata ttctcgaggg ctggcctgga 250
caattactgg ggcttcagcc ttggaaactg gatctgcatt gcatattatg 300
agagcggcta caacaccaca gccccgacgg tcctggatga cggcagcatc 350
gactatggca tcttccagat caacagcttc gcgtggtgca gacgcggaaa 400
gctgaaggag aacaaccact gccatgtcgc ctgctcagcc ttgatcactg 450
atgacctcac agatgcaatt atctgtgcac ggaaaattgt taaagagaca 500
caaggaatga actattggca aggctggaag aaacattgtg agggcagaga 550
cctgtccgag tggaaaaaaag gctgtgaggt ttcctaaact ggaactggac 600
ccaggatgct ttgcagcaac gcccttaggat ttgcagtgaa tgtccaaatg 650
cctgtgtcat cttgtccgt ttcctccaa tattccttct caaacttgaa 700
gagggaaaat taagctatac ttttaagaaa ataaatattt ccatttaat 750
gtc 753

<210> 203
<211> 148
<212> PRT
<213> Homo sapiens

<400> 203

Met	Lys	Ala	Ala	Gly	Ile	Leu	Thr	Leu	Ile	Gly	Cys	Leu	Val	Thr
1					5				10					15

Gly Ala Glu Ser Lys Ile Tyr Thr Arg Cys Lys Leu Ala Lys Ile

	20					25						30		
--	----	--	--	--	--	----	--	--	--	--	--	----	--	--

Phe Ser Arg Ala Gly Leu Asp Asn Tyr Trp Gly Phe Ser Leu Gly

	35					40					45			
--	----	--	--	--	--	----	--	--	--	--	----	--	--	--

Asn Trp Ile Cys Met Ala Tyr Tyr Glu Ser Gly Tyr Asn Thr Thr

	50					55				60				
--	----	--	--	--	--	----	--	--	--	----	--	--	--	--

Ala Pro Thr Val Leu Asp Asp Gly Ser Ile Asp Tyr Gly Ile Phe

	65					70				75				
--	----	--	--	--	--	----	--	--	--	----	--	--	--	--

Gln Ile Asn Ser Phe Ala Trp Cys Arg Arg Gly Lys Leu Lys Glu

	80					85				90				
--	----	--	--	--	--	----	--	--	--	----	--	--	--	--

Asn Asn His Cys His Val Ala Cys Ser Ala Leu Ile Thr Asp Asp

	95					100				105				
--	----	--	--	--	--	-----	--	--	--	-----	--	--	--	--

Leu Thr Asp Ala Ile Ile Cys Ala Arg Lys Ile Val Lys Glu Thr

	110					115				120				
--	-----	--	--	--	--	-----	--	--	--	-----	--	--	--	--

Gln Gly Met Asn Tyr Trp Gln Gly Trp Lys Lys His Cys Glu Gly

	125					130				135				
--	-----	--	--	--	--	-----	--	--	--	-----	--	--	--	--

Arg Asp Leu Ser Glu Trp Lys Lys Gly Cys Glu Val Ser

	140					145								
--	-----	--	--	--	--	-----	--	--	--	--	--	--	--	--

<210> 204
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 204
gcaggcttg aggatgaagg ctgc 24

<210> 205
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 205
ctcattggct gcctggtcac aggc 24

<210> 206
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 206
ccagtcggac aggtctctcc cctc 24

<210> 207
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 207
tcagtgacca aggctgagca ggcg 24

<210> 208
<211> 47
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-47
<223> Synthetic construct.

<400> 208
ctacacttgt tgcaaactgg caaaaatatt ctcgagggct ggcctgg 47

<210> 209
<211> 1648
<212> DNA
<213> Homo sapiens

<400> 209
caggccattt gcatccact gtccttgtt tcggagccag gccacaccgt 50
cctcagcagt gtcatgtgtt aaaaacgcca agctgaatat atcatgcccc 100
tattaaaact tgtacatggc tccccattgg tttttggaga aaagttcaag 150
ctttttacct tggtgtctgc ctgtatccca gtgttcaggc tggctagacg 200
gcggaagaag atcctatttt actgtcactt cccagatctg cttctcacca 250

agagagattc ttttcttaaa cgactataca gggccccaat tgactggata 300
gaggaataca ccacaggcat ggcagactgc atcttagtca acagccagtt 350
cacagctgct gttttaagg aaacattcaa gtccctgtct cacatagacc 400
ctgatgtcct ctatccatct ctaaatgtca ccagcttga ctcagttgtt 450
cctgaaaagc tggatgacct agtccccaaag gggaaaaaat tcctgctgct 500
ctccatcaac agatacgaaa ggaagaaaaa tctgactttg gcactggaag 550
ccctagtaca gctgcgtgga agattgacat cccaaagattt ggagagggtt 600
catctgatcg tggcaggtgg ttatgacgag agagtcctgg agaatgtgga 650
acattatcag gaattgaaga aaatggtcca acagtccgac cttggccagt 700
atgtgacctt cttgaggtct ttctcagaca aacagaaaat ctccctcctc 750
cacagctgca cgtgtgtgct ttacacacca agcaatgagc actttggcat 800
tgtccctctg gaagccatgt acatgcagtg cccagtcatt gctgttaatt 850
cgggtggacc cttggagtcc attgaccaca gtgtcacagg gtttctgtgt 900
gagcctgacc cggtgcactt ctcagaagca atagaaaaagt tcatccgtga 950
accttcctta aaagccacca tgggcctggc tggaaagagcc agagtgaagg 1000
aaaaattttc ccctgaagca tttacagaac agctctaccg atatgttacc 1050
aaactgctgg tataatcaga ttgttttaa gatctccatt aatgtcattt 1100
ttatggattt tagacccagt tttgaaacca aaaaagaaac ctagaatcta 1150
atgcagaaga gatctttaa aaaataaact tgagtcttga atgtgagcca 1200
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tgctcttcgt tctataaatt ttgaatgata ctgtgcctta attggtttc 1400
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ataatgagag caggctatt gtgttccca gattcaatcc accgaagtgt 1500
tcactgtcat ctgttaggaa atttttgtt gtcctgtctt tgcctggatc 1550
catagcgaga gtgctctgta ttttttttaa gataatttgc atttttgcac 1600
actgagat aataaaaggt gtttatcata aaaaaaaaaa aaaaaaaaaa 1648

<210> 210
<211> 323

<212> PRT

<213> Homo sapiens

<400> 210

Met	Pro	Leu	Leu	Lys	Leu	Val	His	Gly	Ser	Pro	Leu	Val	Phe	Gly
1				5					10				15	
Glu	Lys	Phe	Lys	Leu	Phe	Thr	Leu	Val	Ser	Ala	Cys	Ile	Pro	Val
				20				25				30		
Phe	Arg	Leu	Ala	Arg	Arg	Arg	Lys	Lys	Ile	Leu	Phe	Tyr	Cys	His
				35				40				45		
Phe	Pro	Asp	Leu	Leu	Leu	Thr	Lys	Arg	Asp	Ser	Phe	Leu	Lys	Arg
				50				55				60		
Leu	Tyr	Arg	Ala	Pro	Ile	Asp	Trp	Ile	Glu	Glu	Tyr	Thr	Thr	Gly
				65				70				75		
Met	Ala	Asp	Cys	Ile	Leu	Val	Asn	Ser	Gln	Phe	Thr	Ala	Ala	Val
				80				85				90		
Phe	Lys	Glu	Thr	Phe	Lys	Ser	Leu	Ser	His	Ile	Asp	Pro	Asp	Val
				95				100				105		
Leu	Tyr	Pro	Ser	Leu	Asn	Val	Thr	Ser	Phe	Asp	Ser	Val	Val	Pro
				110				115				120		
Glu	Lys	Leu	Asp	Asp	Leu	Val	Pro	Lys	Gly	Lys	Lys	Phe	Leu	Leu
				125				130				135		
Leu	Ser	Ile	Asn	Arg	Tyr	Glu	Arg	Lys	Lys	Asn	Leu	Thr	Leu	Ala
				140				145				150		
Leu	Glu	Ala	Leu	Val	Gln	Leu	Arg	Gly	Arg	Leu	Thr	Ser	Gln	Asp
				155				160				165		
Trp	Glu	Arg	Val	His	Leu	Ile	Val	Ala	Gly	Gly	Tyr	Asp	Glu	Arg
				170				175				180		
Val	Leu	Glu	Asn	Val	Glu	His	Tyr	Gln	Glu	Leu	Lys	Lys	Met	Val
				185				190	"			195		
Gln	Gln	Ser	Asp	Leu	Gly	Gln	Tyr	Val	Thr	Phe	Leu	Arg	Ser	Phe
				200				205				210		
Ser	Asp	Lys	Gln	Lys	Ile	Ser	Leu	Leu	His	Ser	Cys	Thr	Cys	Val
				215				220				225		
Leu	Tyr	Thr	Pro	Ser	Asn	Glu	His	Phe	Gly	Ile	Val	Pro	Leu	Glu
				230				235				240		
Ala	Met	Tyr	Met	Gln	Cys	Pro	Val	Ile	Ala	Val	Asn	Ser	Gly	Gly
				245				250				255		
Pro	Leu	Glu	Ser	Ile	Asp	His	Ser	Val	Thr	Gly	Phe	Leu	Cys	Glu
				260				265				270		

Pro Asp Pro Val His Phe Ser Glu Ala Ile Glu Lys Phe Ile Arg
275 280 285
Glu Pro Ser Leu Lys Ala Thr Met Gly Leu Ala Gly Arg Ala Arg
290 295 300
Val Lys Glu Lys Phe Ser Pro Glu Ala Phe Thr Glu Gln Leu Tyr
305 310 315
Arg Tyr Val Thr Lys Leu Leu Val
320

<210> 211
<211> 1554
<212> DNA
<213> Homo sapiens

<400> 211
gactacgccc atccgagacg tggctccctg ggccgcagaa ccatgttgg 50
cttcgcgatc ttcgccgtta ccttcttgct ggcttggtg ggagccgtgc 100
tctacctcta tccggcttcc agacaagctg caggaattcc agggattact 150
ccaactgaag aaaaagatgg taatcttcca gatattgtga atagtggaaag 200
tttgcatgag ttcctggta atttgcata gagatatggg cctgtggtct 250
ccttctgggt tggcaggcgc ctcgtggta gtttggcac tggatgtgt 300
ctgaaggcagc atatcaatcc caataagaca tcggaccctt ttgaaaccat 350
gctgaagtca ttatataaggat atcaatctgg tggggcagt gtgagtgaaa 400
accacatgag gaaaaaattt gatggaaatg gtgtgactga ttctctgaaag 450
agtaactttg ccctcctcct aaagcttca gaagaattat tagataaattg 500
gctctcctac ccagagaccc agcacgtgcc cctcagccag catatgctt 550
gttttgcata gaagtctgtt acacagatgg taatgggttag tacatggaa 600
gatgatcagg aagtcatcg cttccagaag aatcatggca cagtttggtc 650
tgagattgga aaaggcttc tagatgggtc acttgataaa aacatgactc 700
ggaaaaaaca atatgaagat gccctcatgc aactggagtc tgttttaagg 750
aacatcataa aagaacgaaa aggaagggac ttcaatcaac atatttcat 800
tgactcctta gtacaaggaa accttaatga ccaacagatc ctagaagaca 850
gtatgatatt ttctctggcc agttgcataa taactgcaaa attgtgtacc 900
tggcaatct gtttttaac cacctctgaa gaagttcaaa aaaaattata 950
tgaagagata aaccaagttt ttggaaatgg tcctgttact ccagagaaaa 1000

ttgagcagct cagatattgt cagcatgtgc ttttgaaac tgttcgaact 1050
gccaaactga ctccagttc tgcccagctt caagatattg aaggaaaaat 1100
tgaccgattt attattccta gagagaccct cgtcctttat gcccttggtg 1150
tggtaattca ggatccta atctggccat ctccacacaa gtttgcata 1200
gatcggttg atgatgaatt agtaatgaaa acttttcct cacttggatt 1250
ctcaggcaca caggagtgtc cagagttgag gtttgcata atggtgacca 1300
cagtaattct tagtgtattt gtgaagagac tgcacctact ttctgtggag 1350
ggacaggtta ttgaaacaaa gatgaaactg gtaacatcat caaggaaaga 1400
agcttggatc actgtctcaa agagatatta aaattttata catttaaaat 1450
cattgttaaa ttgattgagg aaaacaacca tttttttttt atctatgtt 1500
aatcctttta taaaccagta tcactttgta atataaacac ctatttgac 1550
ttaa 1554

<210> 212

<211> 462

<212> PRT

<213> Homo sapiens

<400> 212

Met	Leu	Asp	Phe	Ala	Ile	Phe	Ala	Val	Thr	Phe	Leu	Leu	Ala	Leu
1									10					15
Val	Gly	Ala	Val	Leu	Tyr	Leu	Tyr	Pro	Ala	Ser	Arg	Gln	Ala	Ala
									25					30
Gly	Ile	Pro	Gly	Ile	Thr	Pro	Thr	Glu	Glu	Lys	Asp	Gly	Asn	Leu
									40					45
Pro	Asp	Ile	Val	Asn	Ser	Gly	Ser	Leu	His	Glu	Phe	Leu	Val	Asn
									55					60
Leu	His	Glu	Arg	Tyr	Gly	Pro	Val	Val	Ser	Phe	Trp	Phe	Gly	Arg
									70					75
Arg	Leu	Val	Val	Ser	Leu	Gly	Thr	Val	Asp	Val	Leu	Lys	Gln	His
									85					90
Ile	Asn	Pro	Asn	Lys	Thr	Ser	Asp	Pro	Phe	Glu	Thr	Met	Leu	Lys
									95					105
Ser	Leu	Leu	Arg	Tyr	Gln	Ser	Gly	Gly	Ser	Val	Ser	Glu	Asn	
									110					120
His	Met	Arg	Lys	Lys	Leu	Tyr	Glu	Asn	Gly	Val	Thr	Asp	Ser	Leu
									125					135
Lys	Ser	Asn	Phe	Ala	Leu	Leu	Lys	Leu	Ser	Glu	Glu	Leu	Leu	

140	145	150
Asp Lys Trp Leu Ser Tyr Pro Glu Thr Gln His Val Pro Leu Ser		
155	160	165
Gln His Met Leu Gly Phe Ala Met Lys Ser Val Thr Gln Met Val		
170	175	180
Met Gly Ser Thr Phe Glu Asp Asp Gln Glu Val Ile Arg Phe Gln		
185	190	195
Lys Asn His Gly Thr Val Trp Ser Glu Ile Gly Lys Gly Phe Leu		
200	205	210
Asp Gly Ser Leu Asp Lys Asn Met Thr Arg Lys Lys Gln Tyr Glu		
215	220	225
Asp Ala Leu Met Gln Leu Glu Ser Val Leu Arg Asn Ile Ile Lys		
230	235	240
Glu Arg Lys Gly Arg Asn Phe Ser Gln His Ile Phe Ile Asp Ser		
245	250	255
Leu Val Gln Gly Asn Leu Asn Asp Gln Gln Ile Leu Glu Asp Ser		
260	265	270
Met Ile Phe Ser Leu Ala Ser Cys Ile Ile Thr Ala Lys Leu Cys		
275	280	285
Thr Trp Ala Ile Cys Phe Leu Thr Thr Ser Glu Glu Val Gln Lys		
290	295	300
Lys Leu Tyr Glu Glu Ile Asn Gln Val Phe Gly Asn Gly Pro Val		
305	310	315
Thr Pro Glu Lys Ile Glu Gln Leu Arg Tyr Cys Gln His Val Leu		
320	325	330
Cys Glu Thr Val Arg Thr Ala Lys Leu Thr Pro Val Ser Ala Gln		
335	340	345
Leu Gln Asp Ile Glu Gly Lys Ile Asp Arg Phe Ile Ile Pro Arg		
350	355	360
Glu Thr Leu Val Leu Tyr Ala Leu Gly Val Val Leu Gln Asp Pro		
365	370	375
Asn Thr Trp Pro Ser Pro His Lys Phe Asp Pro Asp Arg Phe Asp		
380	385	390
Asp Glu Leu Val Met Lys Thr Phe Ser Ser Leu Gly Phe Ser Gly		
395	400	405
Thr Gln Glu Cys Pro Glu Leu Arg Phe Ala Tyr Met Val Thr Thr		
410	415	420
Val Leu Leu Ser Val Leu Val Lys Arg Leu His Leu Leu Ser Val		
425	430	435

Glu Gly Gln Val Ile Glu Thr Lys Tyr Glu Leu Val Thr Ser Ser
440 445 450

Arg Glu Glu Ala Trp Ile Thr Val Ser Lys Arg Tyr
455 460

<210> 213

<211> 759

<212> DNA

<213> Homo sapiens

<400> 213

ctagatttgt cggcttgcgg ggagacttca ggagtcgctg tctctgaact 50
tccagcctca gagaccgccc cccttgcctcc cgagggccat gggccgggtc 100
tcagggcttg tgccctctcg cttcctgacg ctcctggcgc atctgggtgt 150
cgtcatcacc ttattctggc cccgggacac caacatacag gcctgcctgc 200
ctctcacgtt caccggcag gagtatgaca agcaggacat tcagctggtg 250
gccgcgctct ctgtcaccct gggcctcttt gcagtggagc tggccgggtt 300
cctctcagga gtctccatgt tcaacagcac ccagagcctc atctccattg 350
gggctcactg tagtgcattcc gtggccctgt ccttcttcat attcgagcgt 400
tgggagtgca ctacgtattt gtacatttt gtctctgca gtgcccttcc 450
agctgtcaact gaaatggctt tattcgtcac cgtcttggg ctgaaaaaga 500
aacccttctg attaccttca tgacggaaac ctaaggacga agcctacagg 550
ggcaaggggcc gcttcgtatt ccttggaa ggaaggcata ggcttcgggtt 600
ttccccctcgg aaactgcttc tgcttggagga tatgtgttgg aataattacg 650
tctttagtct gggattatcc gcattgtatt tagtgcattttaataaaaata 700
tgttttgttag taacatataag acttatatac agtttttaggg gacaattaaa 750
aaaaaaaaaa 759

<210> 214

<211> 140

<212> PRT

<213> Homo sapiens

<400> 214

Met Gly Arg Val Ser Gly Leu Val Pro Ser Arg Phe Leu Thr Leu
1 5 10 15

Leu Ala His Leu Val Val Val Ile Thr Leu Phe Trp Ser Arg Asp
20 25 30

Ser Asn Ile Gln Ala Cys Leu Pro Leu Thr Phe Thr Pro Glu Glu
35 40 45

Tyr Asp Lys Gln Asp Ile Gln Leu Val Ala Ala Leu Ser Val Thr
50 55 60
Leu Gly Leu Phe Ala Val Glu Leu Ala Gly Phe Leu Ser Gly Val
65 70 75
Ser Met Phe Asn Ser Thr Gln Ser Leu Ile Ser Ile Gly Ala His
80 85 90
Cys Ser Ala Ser Val Ala Leu Ser Phe Phe Ile Phe Glu Arg Trp
95 100 105
Glu Cys Thr Thr Tyr Trp Tyr Ile Phe Val Phe Cys Ser Ala Leu
110 115 120
Pro Ala Val Thr Glu Met Ala Leu Phe Val Thr Val Phe Gly Leu
125 130 135
Lys Lys Lys Pro Phe
140

.<210> 215

<211> 697

<212> DNA

<213> Homo sapiens

<400> 215

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gaccggcct gctgcagccc catagtgcctc cggaacgagt ggaaggccct 150
ggcatcagag tgcgcctcaggc acctgagcct gcccttacgc tatgtggtgg 200
tatcgcacac ggcgggcagc agctgcaaca ccccccgcctc gtgccagcag 250
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gtggctggaa cttcacgggt gcccactcag gtcacttätg gaaccccatg 400
tccattggca tcagcttcat gggcaactac atggatcggg tgcccacacc 450
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<210> 216

<211> 196

<212> PRT

<213> Homo sapiens

<400> 216

Met	Ser	Arg	Arg	Ser	Met	Leu	Leu	Ala	Trp	Ala	Leu	Pro	Ser	Leu
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Leu	Arg	Leu	Gly	Ala	Ala	Gln	Glu	Thr	Glu	Asp	Pro	Ala	Cys	Cys
					20				25					30
Ser	Pro	Ile	Val	Pro	Arg	Asn	Glu	Trp	Lys	Ala	Leu	Ala	Ser	Glu
					35				40					45
Cys	Ala	Gln	His	Leu	Ser	Leu	Pro	Leu	Arg	Tyr	Val	Val	Val	Ser
					50				55	:				60
His	Thr	Ala	Gly	Ser	Ser	Cys	Asn	Thr	Pro	Ala	Ser	Cys	Gln	Gln
					65				70					75
Gln	Ala	Arg	Asn	Val	Gln	His	Tyr	His	Met	Lys	Thr	Leu	Gly	Trp
					80				85					90
Cys	Asp	Val	Gly	Tyr	Asn	Phe	Leu	Ile	Gly	Glu	Asp	Gly	Leu	Val
					95				100					105
Tyr	Glu	Gly	Arg	Gly	Trp	Asn	Phe	Thr	Gly	Ala	His	Ser	Gly	His
					110				115					120
Leu	Trp	Asn	Pro	Met	Ser	Ile	Gly	Ile	Ser	Phe	Met	Gly	Asn	Tyr
					125				130					135
Met	Asp	Arg	Val	Pro	Thr	Pro	Gln	Ala	Ile	Arg	Ala	Ala	Gln	Gly
					140				145					150
Leu	Leu	Ala	Cys	Gly	Val	Ala	Gln	Gly	Ala	Leu	Arg	Ser	Asn	Tyr
					155				160					165
Val	Leu	Lys	Gly	His	Arg	Asp	Val	Gln	Arg	Thr	Leu	Ser	Pro	Gly
					170				175					180
Asn	Gln	Leu	Tyr	His	Leu	Ile	Gln	Asn	Trp	Pro	His	Tyr	Arg	Ser
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Pro														

<210> 217

<211> 1871

<212> DNA

<213> Homo sapiens

<400> 217

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tctatcttgtt catctgtggc cagcatgtg gtcctccggg ctcagaggac 150
cctgagcgtg atgaccacga gggccagccc cggccccggg tgcctcgaa 200

gcggggccac atctcaccta agtcccgc ccatggccaaat tccactctcc 250
tagggctgct ggccccgcct ggggaggcctt gggcattct tgggcagccc 300
cccaaccgccc cgaaccacag ccccccaccc tcagccaagg tgaagaaaat 350
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tgctcgac agggaaagatt gtggaccatg gcaatggac cttcagcgtc 450
cacttccaaac acaatgccac aggccaggaa aacatctcca tcagcctcgt 500
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aataaagctt gccccggggc a 1871

<210> 218

<211> 252

<212> PRT

<213> Homo sapiens

<400> 218

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Leu	Tyr	Leu	Val	Ile	Cys	Gly	Gln	Asp	Asp	Gly	Pro	Pro	Gly	Ser	
					20				25						30
Glu	Asp	Pro	Glu	Arg	Asp	Asp	His	Glu	Gly	Gln	Pro	Arg	Pro	Arg	
					35				40						45
Val	Pro	Arg	Lys	Arg	Gly	His	Ile	Ser	Pro	Lys	Ser	Arg	Pro	Met	
					50				55						60
Ala	Asn	Ser	Thr	Leu	Leu	Gly	Leu	Leu	Ala	Pro	Pro	Gly	Glu	Ala	
					65				70						75
Trp	Gly	Ile	Leu	Gly	Gln	Pro	Pro	Asn	Arg	Pro	Asn	His	Ser	Pro	
					80				85						90
Pro	Pro	Ser	Ala	Lys	Val	Lys	Lys	Ile	Phe	Gly	Trp	Gly	Asp	Phe	
					95				100						105
Tyr	Ser	Asn	Ile	Lys	Thr	Val	Ala	Leu	Asn	Leu	Leu	Val	Thr	Gly	
					110				115						120
Lys	Ile	Val	Asp	His	Gly	Asn	Gly	Thr	Phe	Ser	Val	His	Phe	Gln	
					125				130						135
His	Asn	Ala	Thr	Gly	Gln	Gly	Asn	Ile	Ser	Ile	Ser	Leu	Val	Pro	
					140				145						150
Pro	Ser	Lys	Ala	Val	Glu	Phe	His	Gln	Glu	Gln	Gln	Ile	Phe	Ile	
					155				160						165
Glu	Ala	Lys	Ala	Ser	Lys	Ile	Phe	Asn	Cys	Arg	Met	Glu	Trp	Glu	
					170				175						180
Lys	Val	Glu	Arg	Gly	Arg	Arg	Thr	Ser	Leu	Cys	Thr	His	Asp	Pro	
					185				190						195
Ala	Lys	Ile	Cys	Ser	Arg	Asp	His	Ala	Gln	Ser	Ser	Ala	Thr	Trp	
					200				205						210

Ser Cys Ser Gln Pro Phe Lys Val Val Cys Val Tyr Ile Ala Phe
215 220 225

Tyr Ser Thr Asp Tyr Arg Leu Val Gln Lys Val Cys Pro Asp Tyr
230 235 240

Asn Tyr His Ser Asp Thr Pro Tyr Tyr Pro Ser Gly
245 250

<210> 219

<211> 2065

<212> DNA

<213> Homo sapiens

<400> 219

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agctcgaggg gagactttga cttcaagcca cagaatttggt ggaagtgtgc 200
gcccgcgc cgcgcgtcgct cctgcagcgc tgtcgaccta gccgctagca 250
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ttcaaatatc ccatactaa atttagtgca atatctgtc ttttgtatag 2000
gtcatatgaa ttcataaaat tattttagtc tgttatagaa taaagattaa 2050
tatatgttaa aaaaa 2065

<210> 220
<211> 201
<212> PRT
<213> Homo sapiens

<400> 220
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Leu Val Leu Thr Leu Pro Gly Leu Pro Val Trp Ala Gln Asn Asp
20 25 30
Thr Glu Pro Ile Val Leu Glu Gly Lys Cys Leu Val Val Cys Asp
35 40 45
Ser Asn Pro Ala Thr Asp Ser Lys Gly Ser Ser Ser Pro Leu
50 55 60

Gly Ile Ser Val Arg Ala Ala Asn Ser Lys Val Ala Phe Ser Ala
 65 70 75
 Val Arg Ser Thr Asn His Glu Pro Ser Glu Met Ser Asn Lys Thr
 80 85 90
 Arg Ile Ile Tyr Phe Asp Gln Ile Leu Val Asn Val Gly Asn Phe
 95 100 105
 Phe Thr Leu Glu Ser Val Phe Val Ala Pro Arg Lys Gly Ile Tyr
 110 115 120
 Ser Phe Ser Phe His Val Ile Lys Val Tyr Gln Ser Gln Thr Ile
 125 130 135
 Gln Val Asn Leu Met Leu Asn Gly Lys Pro Val Ile Ser Ala Phe
 140 145 150
 Ala Gly Asp Lys Asp Val Thr Arg Glu Ala Ala Thr Asn Gly Val
 155 160 165
 Leu Leu Tyr Leu Asp Lys Glu Asp Lys Val Tyr Leu Lys Leu Glu
 170 175 180
 Lys Gly Asn Leu Val Gly Gly Trp Gln Tyr Ser Thr Phe Ser Gly
 185 190 195
 Phe Leu Val Phe Pro Leu
 200

<210> 221
 <211> 20
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-20
 <223> Synthetic construct.

<400> 221
 acggctcacc atgggctccg 20

<210> 222
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 222
 aggaagagga gcccttggag tccg 24

<210> 223
 <211> 40

<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-40
<223> Synthetic construct.

<400> 223
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<210> 224
<211> 902
<212> DNA
<213> Homo sapiens

<400> 224
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tatcatcttc ctcatcgccg gagctttttt ctgggtggtg tctctactga 150
tttcgtccct tgtttggttc atggcaagag tcattattga caacaaagat 200
ggaccaacac agaaatatct gctgatctt ggagcgttt tctctgtcta 250
tatccaagaa atgttccgat ttgcatattta taaactctta aaaaaagcca 300
gtgaagggtt gaagagtata aaccagggtt agacagcacc ctctatgcga 350
ctgctggcct atgtttctgg ctgggctt ggaatcatga gtggagtatt 400
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<210> 225
<211> 257
<212> PRT

<213> Homo sapiens

<400> 225

Met	Thr	Ala	Ala	Val	Phe	Phe	Gly	Cys	Ala	Phe	Ile	Ala	Phe	Gly
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Pro	Ala	Leu	Ala	Leu	Tyr	Val	Phe	Thr	Ile	Ala	Ile	Glu	Pro	Leu
				20					25					30
Arg	Ile	Ile	Phe	Leu	Ile	Ala	Gly	Ala	Phe	Phe	Trp	Leu	Val	Ser
				35					40					45
Leu	Leu	Ile	Ser	Ser	Leu	Val	Trp	Phe	Met	Ala	Arg	Val	Ile	Ile
				50					55					60
Asp	Asn	Lys	Asp	Gly	Pro	Thr	Gln	Lys	Tyr	Leu	Leu	Ile	Phe	Gly
				65					70					75
Ala	Phe	Val	Ser	Val	Tyr	Ile	Gln	Glu	Met	Phe	Arg	Phe	Ala	Tyr
				80					85					90
Tyr	Lys	Leu	Leu	Lys	Lys	Ala	Ser	Glu	Gly	Leu	Lys	Ser	Ile	Asn
				95					100					105
Pro	Gly	Glu	Thr	Ala	Pro	Ser	Met	Arg	Leu	Leu	Ala	Tyr	Val	Ser
				110					115					120
Gly	Leu	Gly	Phe	Gly	Ile	Met	Ser	Gly	Val	Phe	Ser	Phe	Val	Asn
				125					130					135
Thr	Leu	Ser	Asp	Ser	Leu	Gly	Pro	Gly	Thr	Val	Gly	Ile	His	Gly
				140					145					150
Asp	Ser	Pro	Gln	Phe	Phe	Leu	Tyr	Ser	Ala	Phe	Met	Thr	Leu	Val
				155					160					165
Ile	Ile	Leu	Leu	His	Val	Phe	Trp	Gly	Ile	Val	Phe	Phe	Asp	Gly
				170					175					180
Cys	Glu	Lys	Lys	Lys	Trp	Gly	Ile	Leu	Leu	Ile	Val	Leu	Leu	Thr
				185					190					195
His	Leu	Leu	Val	Ser	Ala	Gln	Thr	Phe	Ile	Ser	Ser	Tyr	Tyr	Gly
				200					205					210
Ile	Asn	Leu	Ala	Ser	Ala	Phe	Ile	Ile	Leu	Val	Leu	Met	Gly	Thr
				215					220					225
Trp	Ala	Phe	Leu	Ala	Ala	Gly	Gly	Ser	Cys	Arg	Ser	Leu	Lys	Leu
				230					235					240
Cys	Leu	Leu	Cys	Gln	Asp	Lys	Asn	Phe	Leu	Leu	Tyr	Asn	Gln	Arg
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Ser	Arg													

<210> 226

<211> 3939
<212> DNA
<213> Homo sapiens

<400> 226
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<210> 227

<211> 832

<212> PRT

<213> Homo sapiens

<400> 227

Met Phe Ala Leu Gly Leu Pro Phe Leu Val Leu Leu Val Ala Ser
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Val Glu Ser His Leu Gly Val Leu Gly Pro Lys Asn Val Ser Gln
20 25 30

Lys Asp Ala Glu Phe Glu Arg Thr Tyr Val Asp Glu Val Asn Ser
 35 40 45
 Glu Leu Val Asn Ile Tyr Thr Phe Asn His Thr Val Thr Arg Asn
 50 55 60
 Arg Thr Glu Gly Val Arg Val Ser Val Asn Val Leu Asn Lys Gln
 65 70 75
 Lys Gly Ala Pro Leu Leu Phe Val Val Arg Gln Lys Glu Ala Val
 80 85 90
 Val Ser Phe Gln Val Pro Leu Ile Leu Arg Gly Met Phe Gln Arg
 95 100 105
 Lys Tyr Leu Tyr Gln Lys Val Glu Arg Thr Leu Cys Gln Pro Pro
 110 115 120
 Thr Lys Asn Glu Ser Glu Ile Gln Phe Phe Tyr Val Asp Val Ser
 125 130 135
 Thr Leu Ser Pro Val Asn Thr Thr Tyr Gln Leu Arg Val Ser Arg
 140 145 150
 Met Asp Asp Phe Val Leu Arg Thr Gly Glu Gln Phe Ser Phe Asn
 155 160 165
 Thr Thr Ala Ala Gln Pro Gln Tyr Phe Lys Tyr Glu Phe Pro Glu
 170 175 180
 Gly Val Asp Ser Val Ile Val Lys Val Thr Ser Asn Lys Ala Phe
 185 190 195
 Pro Cys Ser Val Ile Ser Ile Gln Asp Val Leu Cys Pro Val Tyr
 200 205 210
 Asp Leu Asp Asn Asn Val Ala Phe Ile Gly Met Tyr Gln Thr Met
 215 220 225
 Thr Lys Lys Ala Ala Ile Thr Val Gln Arg Lys Asp Phe Pro Ser
 230 235 240
 Asn Ser Phe Tyr Val Val Val Val Lys Thr Glu Asp Gln Ala
 245 250 255
 Cys Gly Gly Ser Leu Pro Phe Tyr Pro Phe Ala Glu Asp Glu Pro
 260 265 270
 Val Asp Gln Gly His Arg Gln Lys Thr Leu Ser Val Leu Val Ser
 275 280 285
 Gln Ala Val Thr Ser Glu Ala Tyr Val Ser Gly Met Leu Phe Cys
 290 295 300
 Leu Gly Ile Phe Leu Ser Phe Tyr Leu Leu Thr Val Leu Leu Ala
 305 310 315
 Cys Trp Glu Asn Trp Arg Gln Lys Lys Lys Thr Leu Leu Val Ala

320	325	330
Ile Asp Arg Ala Cys Pro Glu Ser Gly His	335	340
345		
Asp Ser Phe Pro Gly Ser Ser Pro Tyr Glu	350	355
Gly Tyr Asn Tyr Gly		360
Ser Phe Glu Asn Val Ser Gly Ser Thr Asp	365	370
Gly Leu Val Asp Ser		375
Ala Gly Thr Gly Asp Leu Ser Tyr Gly Tyr	380	385
Gln Gly Arg Ser Phe		390
Glu Pro Val Gly Thr Arg Pro Arg Val Asp	395	400
Ser Met Ser Ser Val		405
Glu Glu Asp Asp Tyr Asp Thr Leu Thr Asp	410	415
Ile Asp Ser Asp Lys		420
Asn Val Ile Arg Thr Lys Gln Tyr Leu Tyr	425	430
Val Ala Asp Leu Ala		435
Arg Lys Asp Lys Arg Val Leu Arg Lys Lys	440	445
Tyr Gln Ile Tyr Phe		450
Trp Asn Ile Ala Thr Ile Ala Val Phe Tyr	455	460
Ala Leu Pro Val Val		465
Gln Leu Val Ile Thr Tyr Gln Thr Val Val	470	475
Asn Val Thr Gly Asn		480
Gln Asp Ile Cys Tyr Tyr Asn Phe Leu Cys	485	490
Ala His Pro Leu Gly		495
Asn Leu Ser Ala Phe Asn Asn Ile Leu Ser	500	505
Asn Leu Gly Tyr Ile		510
Leu Leu Gly Leu Leu Phe Leu Leu Ile Ile	515	520
Leu Gln Arg Glu Ile		525
Asn His Asn Arg Ala Leu Leu Arg Asn Asp	530	535
Leu Cys Ala Leu Glu		540
Cys Gly Ile Pro Lys His Phe Gly Leu Phe	545	550
Tyr Ala Met Gly Thr		555
Ala Leu Met Met Glu Gly Leu Leu Ser Ala	560	565
Cys Tyr His Val Cys		570
Pro Asn Tyr Thr Asn Phe Gln Phe Asp	575	580
Thr Ser Phe Met Tyr Met		585
Ile Ala Gly Leu Cys Met Leu Lys Leu Tyr	590	595
Gln Lys Arg His Pro		600
Asp Ile Asn Ala Ser Ala Tyr Ser Ala Tyr	605	610
Ala Cys Leu Ala Ile		615

Val	Ile	Phe	Phe	Ser	Val	Leu	Gly	Val	Val	Phe	Gly	Lys	Gly	Asn
620														630
Thr	Ala	Phe	Trp	Ile	Val	Phe	Ser	Ile	Ile	His	Ile	Ile	Ala	Thr
635														645
Leu	Leu	Leu	Ser	Thr	Gln	Leu	Tyr	Tyr	Met	Gly	Arg	Trp	Lys	Leu
650														660
Asp	Ser	Gly	Ile	Phe	Arg	Arg	Ile	Leu	His	Val	Leu	Tyr	Thr	Asp
665														675
Cys	Ile	Arg	Gln	Cys	Ser	Gly	Pro	Leu	Tyr	Val	Asp	Arg	Met	Val
680														690
Leu	Leu	Val	Met	Gly	Asn	Val	Ile	Asn	Trp	Ser	Leu	Ala	Ala	Tyr
695														705
Gly	Leu	Ile	Met	Arg	Pro	Asn	Asp	Phe	Ala	Ser	Tyr	Leu	Leu	Ala
710														720
Ile	Gly	Ile	Cys	Asn	Leu	Leu	Leu	Tyr	Phe	Ala	Phe	Tyr	Ile	Ile
725														735
Met	Lys	Leu	Arg	Ser	Gly	Glu	Arg	Ile	Lys	Leu	Ile	Pro	Leu	Leu
740														750
Cys	Ile	Val	Cys	Thr	Ser	Val	Val	Trp	Gly	Phe	Ala	Leu	Phe	Phe
755														765
Phe	Phe	Gln	Gly	Leu	Ser	Thr	Trp	Gln	Lys	Thr	Pro	Ala	Glu	Ser
770														780
Arg	Glu	His	Asn	Arg	Asp	Cys	Ile	Leu	Leu	Asp	Phe	Phe	Asp	Asp
785														795
His	Asp	Ile	Trp	His	Phe	Leu	Ser	Ser	Ile	Ala	Met	Phe	Gly	Ser
800														810
Phe	Leu	Val	Leu	Leu	Thr	Leu	Asp	Asp	Asp	Leu	Asp	Thr	Val	Gln
815														825
Arg	Asp	Lys	Ile	Tyr	Val	Phe								
830														

<210> 228

<211> 2848

<212> DNA

<213> Homo sapiens

<400> 228

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ttggggcgctg gagggcctgt cctgaccatg gtccctgcct ggctgtggct 150

gctttgtgtc tccgtccccc aggctctccc caaggccccag cctgcagagc 200

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<210> 229
<211> 807
<212> PRT
<213> Homo sapiens

<400> 229
Met Val Pro Ala Trp Leu Trp Leu Leu Cys Val Ser Val Pro Gln
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Ala Leu Pro Lys Ala Gln Pro Ala Glu Leu Ser Val Glu Val Pro

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35	40	45
Leu Pro Arg Glu Gly Ala Glu Gly Gln Ile Val Leu Ser Gly Asp		
50	55	60
Ser Gly Lys Ala Thr Glu Gly Pro Phe Ala Met Asp Pro Asp Ser		
65	70	75
Gly Phe Leu Leu Val Thr Arg Ala Leu Asp Arg Glu Glu Gln Ala		
80	85	90
Glu Tyr Gln Leu Gln Val Thr Leu Glu Met Gln Asp Gly His Val		
95	100	105
Leu Trp Gly Pro Gln Pro Val Leu Val His Val Lys Asp Glu Asn		
110	115	120
Asp Gln Val Pro His Phe Ser Gln Ala Ile Tyr Arg Ala Arg Leu		
125	130	135
Ser Arg Gly Thr Arg Pro Gly Ile Pro Phe Leu Phe Leu Glu Ala		
140	145	150
Ser Asp Arg Asp Glu Pro Gly Thr Ala Asn Ser Asp Leu Arg Phe		
155	160	165
His Ile Leu Ser Gln Ala Pro Ala Gln Pro Ser Pro Asp Met Phe		
170	175	180
Gln Leu Glu Pro Arg Leu Gly Ala Leu Ala Leu Ser Pro Lys Gly		
185	190	195
Ser Thr Ser Leu Asp His Ala Leu Glu Arg Thr Tyr Gln Leu Leu		
200	205	210
Val Gln Val Lys Asp Met Gly Asp Gln Ala Ser Gly His Gln Ala		
215	220	225
Thr Ala Thr Val Glu Val Ser Ile Ile Glu Ser Thr Trp Val Ser		
230	235	240
Leu Glu Pro Ile His Leu Ala Glu Asn Leu Lys Val Leu Tyr Pro		
245	250	255
His His Met Ala Gln Val His Trp Ser Gly Gly Asp Val His Tyr		
260	265	270
His Leu Glu Ser His Pro Pro Gly Pro Phe Glu Val Asn Ala Glu		
275	280	285
Gly Asn Leu Tyr Val Thr Arg Glu Leu Asp Arg Glu Ala Gln Ala		
290	295	300
Glu Tyr Leu Leu Gln Val Arg Ala Gln Asn Ser His Gly Glu Asp		
305	310	315

Tyr Ala Ala Pro Leu Glu Leu His Val Leu Val Met Asp Glu Asn
 320 325 330
 Asp Asn Val Pro Ile Cys Pro Pro Arg Asp Pro Thr Val Ser Ile
 335 340 345
 Pro Glu Leu Ser Pro Pro Gly Thr Glu Val Thr Arg Leu Ser Ala
 350 355 360
 Glu Asp Ala Asp Ala Pro Gly Ser Pro Asn Ser His Val Val Tyr
 365 370 375
 Gln Leu Leu Ser Pro Glu Pro Glu Asp Gly Val Glu Gly Arg Ala
 380 385 390
 Phe Gln Val Asp Pro Thr Ser Gly Ser Val Thr Leu Gly Val Leu
 395 400 405
 Pro Leu Arg Ala Gly Gln Asn Ile Leu Leu Leu Val Leu Ala Met
 410 415 420
 Asp Leu Ala Gly Ala Glu Gly Gly Phe Ser Ser Thr Cys Glu Val
 425 430 435
 Glu Val Ala Val Thr Asp Ile Asn Asp His Ala Pro Glu Phe Ile
 440 445 450
 Thr Ser Gln Ile Gly Pro Ile Ser Leu Pro Glu Asp Val Glu Pro
 455 460 465
 Gly Thr Leu Val Ala Met Leu Thr Ala Ile Asp Ala Asp Leu Glu
 470 475 480
 Pro Ala Phe Arg Leu Met Asp Phe Ala Ile Glu Arg Gly Asp Thr
 485 490 495
 Glu Gly Thr Phe Gly Leu Asp Trp Glu Pro Asp Ser Gly His Val
 500 505 510
 Arg Leu Arg Leu Cys Lys Asn Leu Ser Tyr Glu Ala Ala Pro Ser
 515 520 525
 His Glu Val Val Val Val Val Gln Ser Val Ala Lys Leu Val Gly
 530 535 540
 Pro Gly Pro Gly Pro Gly Ala Thr Ala Thr Val Thr Val Leu Val
 545 550 555
 Glu Arg Val Met Pro Pro Pro Lys Leu Asp Gln Glu Ser Tyr Glu
 560 565 570
 Ala Ser Val Pro Ile Ser Ala Pro Ala Gly Ser Phe Leu Leu Thr
 575 580 585
 Ile Gln Pro Ser Asp Pro Ile Ser Arg Thr Leu Arg Phe Ser Leu
 590 595 600
 Val Asn Asp Ser Glu Gly Trp Leu Cys Ile Glu Lys Phe Ser Gly

605	610	615
Glu Val His Thr Ala Gln Ser Leu Gln	Gly Ala Gln Pro Gly Asp	
620	625	630
Thr Tyr Thr Val Leu Val Glu Ala Gln	Asp Thr Ala Leu Thr Leu	
635	640	645
Ala Pro Val Pro Ser Gln Tyr Leu Cys	Thr Pro Arg Gln Asp His	
650	655	660
Gly Leu Ile Val Ser Gly Pro Ser Lys	Asp Pro Asp Leu Ala Ser	
665	670	675
Gly His Gly Pro Tyr Ser Phe Thr Leu	Gly Pro Asn Pro Thr Val	
680	685	690
Gln Arg Asp Trp Arg Leu Gln Thr Leu	Asn Gly Ser His Ala Tyr	
695	700	705
Leu Thr Leu Ala Leu His Trp Val Glu	Pro Arg Glu His Ile Ile	
710	715	720
Pro Val Val Val Ser His Asn Ala Gln	Met Trp Gln Leu Leu Val	
725	730	735
Arg Val Ile Val Cys Arg Cys Asn Val	Glu Gly Gln Cys Met Arg	
740	745	750
Lys Val Gly Arg Met Lys Gly Met Pro	Thr Lys Leu Ser Ala Val	
755	760	765
Gly Ile Leu Val Gly Thr Leu Val Ala	Ile Gly Ile Phe Leu Ile	
770	775	780
Leu Ile Phe Thr His Trp Thr Met Ser	Arg Lys Lys Asp Pro Asp	
785	790	795
Gln Pro Ala Asp Ser Val Pro Leu Lys	Ala Thr Val	
800	805	

<210> 230

<211> 50

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-50

<223> Synthetic construct.

<400> 230

cgccttaccc cgccagcccg a gatttca tggtgaaaat cgccttcaat 50

<210> 231

<211> 24

<212> DNA

<213> Artificial Sequence

<220>
<221> Artificial Sequence
<222> full
<223> Synthetic oligonucleotide probe

<400> 231
cctgagctgt aaccccaactc cagg 24

<210> 232
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 232
agagtctgtc ccagctatct tgt 23

<210> 233
<211> 2786
<212> DNA
<213> Homo sapiens

<400> 233
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cagaaatgga gacgagatca gcaaattgag tcaactatgt aattcaaaca 150
acttgaagct caatttctgg aaatctccct ctccttcaa tcggcctgtg 200
gatgtcctgg tcccatctgt cagtctgcag gcatttaat cttcctgag 250
atcccagggc ttagagtacg cagtgacaat tgaggacctg caggcccttt 300
tagacaatga agatgatgaa atgcaacaca atgaagggcg agaacggagc 350
agtaataact tcaactacgg ggcttaccat tcccttggaa ctatccatca 400
cgagatggac aacattgccg cagactttcc tgacctggcg aggagggtga 450
agattggaca ttctttgaa aaccggccga tgtatgtact gaagttcagc 500
actggaaag gcgtgaggcg gccggccgtt tggctgaatg caggcatcca 550
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<210> 234

<211> 421

<212> PRT

<213> Homo sapiens

<400> 234

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Val Arg Asn Gly Asp Glu Ile Ser Lys Leu Ser Gln Leu Val Asn
35 40 45

Ser Asn Asn Leu Lys Leu Asn Phe Trp Lys Ser Pro Ser Ser Phe
50 55 60

Asn Arg Pro Val Asp Val Leu Val Pro Ser Val Ser Leu Gln Ala
65 70 75

Phe Lys Ser Phe Leu Arg Ser Gln Gly Leu Glu Tyr Ala Val Thr
80 85 90

Ile Glu Asp Leu Gln Ala Leu Leu Asp Asn Glu Asp Asp Glu Met
95 100 105

Gln His Asn Glu Gln Gln Glu Arg Ser Ser Asn Asn Phe Asn Tyr
110 115 120

Gly Ala Tyr His Ser Leu Glu Ala Ile Tyr His Glu Met Asp Asn
125 130 135

Ile Ala Ala Asp Phe Pro Asp Leu Ala Arg Arg Val Lys Ile Gly
140 145 150

His Ser Phe Glu Asn Arg Pro Met Tyr Val Leu Lys Phe Ser Thr
155 160 165

Gly Lys Gly Val Arg Arg Pro Ala Val Trp Leu Asn Ala Gly Ile
 170 175 180
 His Ser Arg Glu Trp Ile Ser Gln Ala Thr Ala Ile Trp Thr Ala
 185 190 195
 Arg Lys Ile Val Ser Asp Tyr Gln Arg Asp Pro Ala Ile Thr Ser
 200 205 210
 Ile Leu Glu Lys Met Asp Ile Phe Leu Leu Pro Val Ala Asn Pro
 215 220 225
 Asp Gly Tyr Val Tyr Thr Gln Thr Gln Asn Arg Leu Trp Arg Lys
 230 235 240
 Thr Arg Ser Arg Asn Pro Gly Ser Ser Cys Ile Gly Ala Asp Pro
 245 250 255
 Asn Arg Asn Trp Asn Ala Ser Phe Ala Gly Lys Gly Ala Ser Asp
 260 265 270
 Asn Pro Cys Ser Glu Val Tyr His Gly Pro His Ala Asn Ser Glu
 275 280 285
 Val Glu Val Lys Ser Val Val Asp Phe Ile Gln Lys His Gly Asn
 290 295 300
 Phe Lys Gly Phe Ile Asp Leu His Ser Tyr Ser Gln Leu Leu Met
 305 310 315
 Tyr Pro Tyr Gly Tyr Ser Val Lys Lys Ala Pro Asp Ala Glu Glu
 320 325 330
 Leu Asp Lys Val Ala Arg Leu Ala Ala Lys Ala Leu Ala Ser Val
 335 340 345
 Ser Gly Thr Glu Tyr Gln Val Gly Pro Thr Cys Thr Thr Val Tyr
 350 355 360
 Pro Ala Ser Gly Ser Ser Ile Asp Trp Ala Tyr Asp Asn Gly Ile
 365 370 375
 Lys Phe Ala Phe Thr Phe Glu Leu Arg Asp Thr Gly Thr Tyr Gly
 380 385 390
 Phe Leu Leu Pro Ala Asn Gln Ile Ile Pro Thr Ala Glu Glu Thr
 395 400 405
 Trp Leu Gly Leu Lys Thr Ile Met Glu His Val Arg Asp Asn Leu
 410 415 420

Tyr

<210> 235
 <211> 1743
 <212> DNA
 <213> Homo sapiens

<400> 235
caaccatgcaggacaggcaggagaagaggaacctgcaaagacatattt 50
tggcatcttaccttatggatgactcttgctgtggcct 100
atctactgtgtgtccccggccatgcccccagtgcataacc 150
cccgccttcctccacaaagagcaccctgcctcacaggtgtattccctc 200
aacaccgactttgccttccgcctataaccgcaggctggtttggagacccc 250
gagtcagaacatcttcttcccctgtgagtgtctccacttccctggcca 300
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ccagcacctggttactcacactgttcccagcaaagacctgaccttga 450
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aatcacaaa ccatcaacag ggacccagt cacaagccaa cacccattaa 1500
ccccagtcag tgccctttc cacaattct cccaggtaac tagcttcatg 1550
ggatgttgct gggttaccat attccattc cttggggctc ccaggaatgg 1600
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attcaataaa actaaaatat gaattcaaaa aaaaaaaaaa aaaaaaaaaa 1700
aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 1743

<210> 236
<211> 417
<212> PRT
<213> Homo sapiens

<400> 236

Met	Ala	Ser	Tyr	Leu	Tyr	Gly	Val	Leu	Phe	Ala	Val	Gly	Leu	Cys
1				5				10					15	
Ala	Pro	Ile	Tyr	Cys	Val	Ser	Pro	Ala	Asn	Ala	Pro	Ser	Ala	Tyr
	20					25							30	
Pro	Arg	Pro	Ser	Ser	Thr	Lys	Ser	Thr	Pro	Ala	Ser	Gln	Val	Tyr
		35					40						45	
Ser	Leu	Asn	Thr	Asp	Phe	Ala	Phe	Arg	Leu	Tyr	Arg	Arg	Leu	Val
		50					55						60	
Leu	Glu	Thr	Pro	Ser	Gln	Asn	Ile	Phe	Phe	Ser	Pro	Val	Ser	Val
		65						70					75	
Ser	Thr	Ser	Leu	Ala	Met	Leu	Ser	Leu	Gly	Ala	His	Ser	Val	Thr
		80					85						90	
Lys	Thr	Gln	Ile	Leu	Gln	Gly	Leu	Gly	Phe	Asn	Leu	Thr	His	Thr
		95					100						105	
Pro	Glu	Ser	Ala	Ile	His	Gln	Gly	Phe	Gln	His	Leu	Val	His	Ser
		110					115						120	
Leu	Thr	Val	Pro	Ser	Lys	Asp	Leu	Thr	Leu	Lys	Met	Gly	Ser	Ala
		125					130						135	
Leu	Phe	Val	Lys	Lys	Glu	Leu	Gln	Leu	Gln	Ala	Asn	Phe	Leu	Gly
		140					145						150	
Asn	Val	Lys	Arg	Leu	Tyr	Glu	Ala	Glu	Val	Phe	Ser	Thr	Asp	Phe
		155					160						165	
Ser	Asn	Pro	Ser	Ile	Ala	Gln	Ala	Arg	Ile	Asn	Ser	His	Val	Lys
		170					175						180	
Lys	Lys	Thr	Gln	Gly	Lys	Val	Val	Asp	Ile	Ile	Gln	Gly	Leu	Asp
		185					190						195	
Leu	Leu	Thr	Ala	Met	Val	Leu	Val	Asn	His	Ile	Phe	Phe	Lys	Ala

200	205	210
Lys Trp Glu Lys Pro Phe His Leu Glu	Tyr Thr Arg Lys Asn Phe	
215	220	225
Pro Phe Leu Val Gly Glu Gln Val Thr Val Gln Val Pro Met Met		
230	235	240
His Gln Lys Glu Gln Phe Ala Phe Gly Val Asp Thr Glu Leu Asn		
245	250	255
Cys Phe Val Leu Gln Met Asp Tyr Lys Gly Asp Ala Val Ala Phe		
260	265	270
Phe Val Leu Pro Ser Lys Gly Lys Met Arg Gln Leu Glu Gln Ala		
275	280	285
Leu Ser Ala Arg Thr Leu Ile Lys Trp Ser His Ser Leu Gln Lys		
290	295	300
Arg Trp Ile Glu Val Phe Ile Pro Arg Phe Ser Ile Ser Ala Ser		
305	310	315
Tyr Asn Leu Glu Thr Ile Leu Pro Lys Met Gly Ile Gln Asn Ala		
320	325	330
Phe Asp Lys Asn Ala Asp Phe Ser Gly Ile Ala Lys Arg Asp Ser		
335	340	345
Leu Gln Val Ser Lys Ala Thr His Lys Ala Val Leu Asp Val Ser		
350	355	360
Glu Glu Gly Thr Glu Ala Thr Ala Ala Thr Thr Thr Lys Phe Ile		
365	370	375
Val Arg Ser Lys Asp Gly Pro Ser Tyr Phe Thr Val Ser Phe Asn		
380	385	390
Arg Thr Phe Leu Met Met Ile Thr Asn Lys Ala Thr Asp Gly Ile		
395	400	405
Leu Phe Leu Gly Lys Val Glu Asn Pro Thr Lys Ser		
410	415	

<210> 237
 <211> 23
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-23
 <223> Synthetic construct.

<400> 237
 caaccatgca aggacagggc agg 23

<210> 238

<211> 47
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-47
<223> Synthetic construct.

<400> 238
ctttgctgtt ggcctctgtg ctcccaacca tgcaaggaca gggcagg 47

<210> 239
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 239
tgactcgggg tctccaaaac cagc 24

<210> 240
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 240
ggtataggcg gaaggcaaag tcgg 24

<210> 241
<211> 48
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-48
<223> Synthetic construct.

<400> 241
ggcatttac ctatggag tactcttgc tggcgtcc 48

<210> 242
<211> 2436
<212> DNA
<213> Homo sapiens

<400> 242
ggctgaccgt gctacattgc ctggaggaag cctaaaggaaac ccaggcatcc 50

agctgcccac gcctgagtcc aagattcttc ccaggaacac aaacgttagga 100
gacccacgct cctggaagca ccagcctta tctcttcacc ttcaagtccc 150
ctttctcaag aatcctctgt tctttgcctt ctaaagtctt ggtacatcta 200
ggacccaggc atcttgctt ccagccacaa agagacagat gaagatgcag 250
aaaggaaatg ttctccttat gtttggtcta ctattgcatt tagaagctgc 300
aacaattcc aatgagacta gcacctctgc caacactgga tccagtgtga 350
tctccagtgg agccagcaca gccaccaact ctgggtccag tgtgacctcc 400
agtggggtca gcacagccac catctcaggg tccagcgtga cctccaatgg 450
ggtcagcata gtcaccaact ctgagttcca tacaacctcc agtgggatca 500
gcacagccac caactctgag ttcagcacag cgtccagtgg gatcagcata 550
gccaccaact ctgagtcag cacaacctcc agtggggcca gcacagccac 600
caactctgag tccagcacac cctccagtgg ggccagcaca gtcaccaact 650
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gcacagccac caactctgag tccagaacga cctccaatgg ggctggcaca 1000
gccaccaact ctgagtcag cacgacctcc agtggggcca gcacagccac 1050
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aaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa aaaaaaa 2436

<210> 243

<211> 596

<212> PRT

<213> Homo sapiens

<400> 243

Met	Lys	Met	Gln	Lys	Gly	Asn	Val	Leu	Leu	Met	Phe	Gly	Leu	Leu
1				5				10					15	
Leu	His	Leu	Glu	Ala	Ala	Thr	Asn	Ser	Asn	Glu	Thr	Ser	Thr	Ser
				20				25					30	
Ala	Asn	Thr	Gly	Ser	Ser	Val	Ile	Ser	Ser	Gly	Ala	Ser	Thr	Ala
				35				40					45	
Thr	Asn	Ser	Gly	Ser	Ser	Val	Thr	Ser	Ser	Gly	Val	Ser	Thr	Ala
				50				55					60	
Thr	Ile	Ser	Gly	Ser	Ser	Val	Thr	Ser	Asn	Gly	Val	Ser	Ile	Val
				65				70					75	

Thr Asn Ser Glu Phe His Thr Thr Ser Ser Gly Ile Ser Thr Ala
 80 85 90
 Thr Asn Ser Glu Phe Ser Thr Ala Ser Ser Gly Ile Ser Ile Ala
 95 100 105
 Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala
 110 115 120
 Thr Asn Ser Glu Ser Ser Thr Pro Ser Ser Gly Ala Ser Thr Val
 125 130 135
 Thr Asn Ser Gly Ser Ser Val Thr Ser Ser Gly Ala Ser Thr Ala
 140 145 150
 Thr Asn Ser Glu Ser Ser Thr Val Ser Ser Arg Ala Ser Thr Ala
 155 160 165
 Thr Asn Ser Glu Ser Ser Thr Leu Ser Ser Gly Ala Ser Thr Ala
 170 175 180
 Thr Asn Ser Asp Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala
 185 190 195
 Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala
 200 205 210
 Thr Asn Ser Glu Ser Ser Thr Val Ser Ser Arg Ala Ser Thr Ala
 215 220 225
 Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala
 230 235 240
 Thr Asn Ser Glu Ser Arg Thr Thr Ser Asn Gly Ala Gly Thr Ala
 245 250 255
 Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala
 260 265 270
 Thr Asn Ser Asp Ser Ser Thr Val Ser Ser Gly Ala Ser Thr Ala
 275 280 285
 Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala
 290 295 300
 Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala
 305 310 315
 Thr Asn Ser Asp Ser Ser Thr Thr Ser Ser Gly Ala Gly Thr Ala
 320 325 330
 Thr Asn Ser Glu Ser Ser Thr Val Ser Ser Gly Ile Ser Thr Val
 335 340 345
 Thr Asn Ser Glu Ser Ser Thr Pro Ser Ser Gly Ala Asn Thr Ala
 350 355 360
 Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Asn Thr Ala

365

370

375

Thr Asn Ser Glu Ser Ser Thr Val Ser Ser Gly Ala Ser Thr Ala
380 385 390

Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Val Ser Thr Ala
395 400 405

Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala
410 415 420

Thr Asn Ser Asp Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala
425 430 435

Thr Asn Ser Glu Ser Ser Thr Val Ser Ser Gly Ile Ser Thr Val
440 445 450

Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Asn Thr Ala
455 460 465

Thr Asn Ser Gly Ser Ser Val Thr Ser Ala Gly Ser Gly Thr Ala
470 475 480

Ala Leu Thr Gly Met His Thr Thr Ser His Ser Ala Ser Thr Ala
485 490 495

Val Ser Glu Ala Lys Pro Gly Gly Ser Leu Val Pro Trp Glu Ile
500 505 510

Phe Leu Ile Thr Leu Val Ser Val Val Ala Ala Val Gly Leu Phe
515 520 525

Ala Gly Leu Phe Phe Cys Val Arg Asn Ser Leu Ser Leu Arg Asn
530 535 540

Thr Phe Asn Thr Ala Val Tyr His Pro His Gly Leu Asn His Gly
545 550 555

Leu Gly Pro Gly Pro Gly Gly Asn His Gly Ala Pro His Arg Pro
560 565 570

Arg Trp Ser Pro Asn Trp Phe Trp Arg Arg Pro Val Ser Ser Ile
575 580 585

Ala Met Glu Met Ser Gly Arg Asn Ser Gly Pro
590 595

<210> 244

<211> 26

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-26

<223> Synthetic construct.

<400> 244

gaagcaccag ccttatctc ttcacc 26
<210> 245
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic sequence.

<400> 245
gtcagagttg gtggctgtgc tagc 24

<210> 246
<211> 48
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-48
<223> Synthetic construct.

<400> 246
ggaccaggc atcttgcttt ccagccacaa agagacagat gaagatgc 48

<210> 247
<211> 957
<212> DNA
<213> Homo sapiens

<400> 247
gggagagagg ataaatagca gcgtggcttc cctggctcct ctctgcattcc 50
ttcccgacct tcccagcaat atgcatttg cacgtctggc cggctcctgc 100
tccctccttc tgctactggg ggcctgtct ggatggcgg ccagcgatga 150
ccccatttag aaggtaattt aaggatcaa ccgagggctg agcaatgcag 200
agagagaggt gggcaaggcc ctggatggca tcaacagtgg aatcacgcat 250
gccggaagg aagtggagaa ggtttcaac ggacttagca acatggggag 300
ccacaccggc aaggagttgg acaaaggcgt ccagggctc aaccacggca 350
tggacaagg tggccatgag atcaaccatg gtattggaca agcaggaaag 400
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gaaggaagca gacaaagcgg tccaagggtt ccacactggg gtccaccagg 500
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ccagcaagga ggccaaaccag ctgctgaatg gcaaccatca aagcggatct 700
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gttgtcacat cagctgacat gacctggagg ggttgggggt gggggacagg 900
tttctgaaat ccctgaaggg ggttgtactg ggatttgtga ataaacttga 950
tacacca 957

<210> 248

<211> 247

<212> PRT

<213> Homo sapiens

<400> 248

Met	His	Leu	Ala	Arg	Leu	Val	Gly	Ser	Cys	Ser	Leu	Leu	Leu	Leu
1					5				10					15
Leu	Gly	Ala	Leu	Ser	Gly	Trp	Ala	Ala	Ser	Asp	Asp	Pro	Ile	Glu
					20				25					30
Lys	Val	Ile	Glu	Gly	Ile	Asn	Arg	Gly	Leu	Ser	Asn	Ala	Glu	Arg
					35				40					45
Glu	Val	Gly	Lys	Ala	Leu	Asp	Gly	Ile	Asn	Ser	Gly	Ile	Thr	His
					50				55					60
Ala	Gly	Arg	Glu	Val	Glu	Lys	Val	Phe	Asn	Gly	Leu	Ser	Asn	Met
					65				70					75
Gly	Ser	His	Thr	Gly	Lys	Glu	Leu	Asp	Lys	Gly	Val	Gln	Gly	Leu
					80				85					90
Asn	His	Gly	Met	Asp	Lys	Val	Ala	His	Glu	Ile	Asn	His	Gly	Ile
					95				100					105
Gly	Gln	Ala	Gly	Lys	Glu	Ala	Glu	Lys	Leu	Gly	His	Gly	Val	Asn
					110				115					120
Asn	Ala	Ala	Gly	Gln	Ala	Gly	Lys	Glu	Ala	Asp	Lys	Ala	Val	Gln
					125				130					135
Gly	Phe	His	Thr	Gly	Val	His	Gln	Ala	Gly	Lys	Glu	Ala	Glu	Lys
					140				145					150
Leu	Gly	Gln	Gly	Val	Asn	His	Ala	Ala	Asp	Gln	Ala	Gly	Lys	Glu
					155				160					165
Val	Glu	Lys	Leu	Gly	Gln	Gly	Ala	His	His	Ala	Ala	Gly	Gln	Ala
					170				175					180

Gly Lys Glu Leu Gln Asn Ala His Asn Gly Val Asn Gln Ala Ser
185 190 195
Lys Glu Ala Asn Gln Leu Leu Asn Gly Asn His Gln Ser Gly Ser
200 205 210
Ser Ser His Gln Gly Gly Ala Thr Thr Pro Leu Ala Ser Gly
215 220 225
Ala Ser Val Asn Thr Pro Phe Ile Asn Leu Pro Ala Leu Trp Arg
230 235 240
Ser Val Ala Asn Ile Met Pro
245

<210> 249

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 249

caatatgcattt cttgcacgtc tgg 23

<210> 250

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 250

aagcttctctt gcttcctttc ctgc 24

<210> 251

<211> 43

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-43

<223> Synthetic construct.

<400> 251

tgacccttattt gagaagggtca ttgaagggtt caaccgaggg ctg 43

<210> 252

<211> 3781

<212> DNA

<213> Homo sapiens

<400> 252
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cagtggacac tccaggaaga gcggcccccgc ggggggcgat gaccgtgcgc 100
tgaccctgac tcactccagg tccggagggcg gggggcccccgc gggcgactcg 150
ggggcggacc gcggggcgga gctgcccccgttgagtcgg ccgagccacc 200
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<212> PRT
<213> Homo sapiens

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35 40 45
Pro Arg Ile Ser Leu Pro Leu Gly Ser Glu Glu Arg Pro Phe Leu
50 55 60
Arg Phe Glu Ala Glu His Ile Ser Asn Tyr Thr Ala Leu Leu Leu
65 70 75
Ser Arg Asp Gly Arg Thr Leu Tyr Val Gly Ala Arg Glu Ala Leu

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Phe Ala Leu Ser Ser Asn Leu Ser Phe	Leu Pro Gly Gly Glu	Tyr
95	100	105
Gln Glu Leu Leu Trp Gly Ala Asp Ala	Glu Lys Lys Gln Gln	Cys
110	115	120
Ser Phe Lys Gly Lys Asp Pro Gln Arg	Asp Cys Gln Asn Tyr	Ile
125	130	135
Lys Ile Leu Leu Pro Leu Ser Gly Ser	His Leu Phe Thr Cys	Gly
140	145	150
Thr Ala Ala Phe Ser Pro Met Cys Thr	Tyr Ile Asn Met Glu Asn	
155	160	165
Phe Thr Leu Ala Arg Asp Glu Lys Gly	Asn Val Leu Leu Glu Asp	
170	175	180
Gly Lys Gly Arg Cys Pro Phe Asp Pro	Asn Phe Lys Ser Thr Ala	
185	190	195
Leu Val Val Asp Gly Glu Leu Tyr Thr	Gly Thr Val Ser Ser Phe	
200	205	210
Gln Gly Asn Asp Pro Ala Ile Ser Arg	Ser Gln Ser Leu Arg Pro	
215	220	225
Thr Lys Thr Glu Ser Ser Leu Asn Trp	Leu Gln Asp Pro Ala Phe	
230	235	240
Val Ala Ser Ala Tyr Ile Pro Glu Ser	Leu Gly Ser Leu Gln Gly	
245	250	255
Asp Asp Asp Lys Ile Tyr Phe Phe Ser	Glu Thr Gly Gln Glu	
260	265	270
Phe Glu Phe Phe Glu Asn Thr Ile Val	Ser Arg Ile Ala Arg Ile	
275	280	285
Cys Lys Gly Asp Glu Gly Glu Arg Val	Leu Gln Gln Arg Trp	
290	295	300
Thr Ser Phe Leu Lys Ala Gln Leu Leu	Cys Ser Arg Pro Asp Asp	
305	310	315
Gly Phe Pro Phe Asn Val Leu Gln Asp	Val Phe Thr Leu Ser Pro	
320	325	330
Ser Pro Gln Asp Trp Arg Asp Thr Leu	Phe Tyr Gly Val Phe Thr	
335	340	345
Ser Gln Trp His Arg Gly Thr Thr Glu	Gly Ser Ala Val Cys Val	
350	355	360
Phe Thr Met Lys Asp Val Gln Arg Val	Phe Ser Gly Leu Tyr Lys	
365	370	375

Glu Val Asn Arg Glu Thr Gln Gln Trp Tyr Thr Val Thr His Pro
 380 385 390
 Val Pro Thr Pro Arg Pro Gly Ala Cys Ile Thr Asn Ser Ala Arg
 395 400 405
 Glu Arg Lys Ile Asn Ser Ser Leu Gln Leu Pro Asp Arg Val Leu
 410 415 420
 Asn Phe Leu Lys Asp His Phe Leu Met Asp Gly Gln Val Arg Ser
 425 430 435
 Arg Met Leu Leu Leu Gln Pro Gln Ala Arg Tyr Gln Arg Val Ala
 440 445 450
 Val His Arg Val Pro Gly Leu His His Thr Tyr Asp Val Leu Phe
 455 460 465
 Leu Gly Thr Gly Asp Gly Arg Leu His Lys Ala Val Ser Val Gly
 470 475 480
 Pro Arg Val His Ile Ile Glu Glu Leu Gln Ile Phe Ser Ser Gly
 485 490 495
 Gln Pro Val Gln Asn Leu Leu Leu Asp Thr His Arg Gly Leu Leu
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 Tyr Ala Ala Ser His Ser Gly Val Val Gln Val Pro Met Ala Asn
 515 520 525
 Cys Ser Leu Tyr Arg Ser Cys Gly Asp Cys Leu Leu Ala Arg Asp
 530 535 540
 Pro Tyr Cys Ala Trp Ser Gly Ser Ser Cys Lys His Val Ser Leu
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 Tyr Gln Pro Gln Leu Ala Thr Arg Pro Trp Ile Gln Asp Ile Glu
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 575 580 585
 Pro Ser Phe Val Pro Thr Gly Glu Lys Pro Cys Glu Gln Val Gln
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 605 610 615
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 Ala Ser Ala Ser Cys His Val Leu Pro Thr Gly Asp Leu Leu Leu
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 Val Gly Thr Gln Gln Leu Gly Glu Phe Gln Cys Trp Ser Leu Glu
 650 655 660
 Glu Gly Phe Gln Gln Leu Val Ala Ser Tyr Cys Pro Glu Val Val

665	670	675
Glu Asp Gly Val Ala Asp Gln Thr Asp	Glu Gly Gly Ser Val	Pro
680	685	690
Val Ile Ile Ser Thr Ser Arg Val Ser	Ala Pro Ala Gly Gly	Lys
695	700	705
Ala Ser Trp Gly Ala Asp Arg Ser Tyr	Trp Lys Glu Phe Leu	Val
710	715	720
Met Cys Thr Leu Phe Val Leu Ala Val	Leu Leu Pro Val Leu	Phe
725	730	735
Leu Leu Tyr Arg His Arg Asn Ser Met	Lys Val Phe Leu Lys	Gln
740	745	750
Gly Glu Cys Ala Ser Val His Pro Lys	Thr Cys Pro Val Val	Leu
755	760	765
Pro Pro Glu Thr Arg Pro Leu Asn Gly	Leu Gly Pro Pro Ser	Thr
770	775	780
Pro Leu Asp His Arg Gly Tyr Gln Ser	Leu Ser Asp Ser Pro	Pro
785	790	795
Gly Ala Arg Val Phe Thr Glu Ser Glu	Lys Arg Pro Leu Ser	Ile
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Gln Asp Ser Phe Val Glu Val Ser Pro	Val Cys Pro Arg Pro	Arg
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<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 254

agcccggtgca gaatctgctc ctgg 24

<210> 255

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 255
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<210> 256
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<212> DNA
<213> Artificial

<220>
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<222> 1-18
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<400> 256
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<210> 257
<211> 41
<212> DNA
<213> Artificial

<220>
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<223> Synthetic construct.

<400> 257
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<211> 45
<212> DNA
<213> Artificial

<220>
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<223> Synthetic construct.

<400> 258
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<210> 259
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<212> DNA
<213> Homo sapiens

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<222> 3635
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<400> 259
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<210> 260
<211> 802
<212> PRT
<213> Homo sapiens

<400> 260

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Ala	Ser	Glu	Leu	Lys	Arg	Ala	Gly	Pro	Arg	Arg	Arg	Ala	Ser	Pro
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Glu	Gly	Cys	Arg	Ser	Gly	Gln	Ala	Ala	Ala	Ser	Gln	Ala	Gly	Gly
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Ala	Arg	Gly	Asp	Ala	Arg	Gly	Ala	Gln	Leu	Trp	Pro	Pro	Gly	Ser
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Asp	Pro	Asp	Gly	Gly	Pro	Arg	Asp	Arg	Asn	Phe	Leu	Phe	Val	Gly
		80				85							90	
Val	Met	Thr	Ala	Gln	Lys	Tyr	Leu	Gln	Thr	Arg	Ala	Val	Ala	Ala
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Tyr	Arg	Thr	Trp	Ser	Lys	Thr	Ile	Pro	Gly	Lys	Val	Gln	Phe	Phe
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Ser	Ser	Glu	Gly	Ser	Asp	Thr	Ser	Val	Pro	Ile	Pro	Val	Val	Pro
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Leu	Arg	Gly	Val	Asp	Asp	Ser	Tyr	Pro	Pro	Gln	Lys	Lys	Ser	Phe
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Met	Met	Leu	Lys	Tyr	Met	His	Asp	His	Tyr	Leu	Asp	Lys	Tyr	Glu
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Trp	Phe	Met	Arg	Ala	Asp	Asp	Asp	Val	Tyr	Ile	Lys	Gly	Asp	Arg
		170					175						180	
Leu	Glu	Asn	Phe	Leu	Arg	Ser	Leu	Asn	Ser	Ser	Glu	Pro	Leu	Phe
		185					190						195	
Leu	Gly	Gln	Thr	Gly	Leu	Gly	Thr	Thr	Glu	Glu	Met	Gly	Lys	Leu
		200					205						210	
Ala	Leu	Glu	Pro	Gly	Glu	Asn	Phe	Cys	Met	Gly	Gly	Pro	Gly	Val
		215					220						225	
Ile	Met	Ser	Arg	Glu	Val	Leu	Arg	Arg	Met	Val	Pro	His	Ile	Gly
		230					235						240	

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 Gly Arg Cys Val Arg Arg Phe Ala Gly Val Gln Cys Val Trp Ser
 260 265 270
 Tyr Glu Met Arg Gln Leu Phe Tyr Glu Asn Tyr Glu Gln Asn Lys
 275 280 285
 Lys Gly Tyr Ile Arg Asp Leu His Asn Ser Lys Ile His Gln Ala
 290 295 300
 Ile Thr Leu His Pro Asn Lys Asn Pro Pro Tyr Gln Tyr Arg Leu
 305 310 315
 His Ser Tyr Met Leu Ser Arg Lys Ile Ser Glu Leu Arg His Arg
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 Thr Ile Gln Leu His Arg Glu Ile Val Leu Met Ser Lys Tyr Ser
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 365 370 375
 Trp Glu Phe Leu Thr Gly Lys Tyr Leu Tyr Ser Ala Val Asp Gly
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 485 490 495
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Lys Thr Cys Leu Ile Pro Asn Gln Asn	Val Lys Leu Val Val Leu	
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Leu Phe Asn Ser Asp Ser Asn Pro Asp	Lys Ala Lys Gln Val Glu	
575	580	585
Leu Met Arg Asp Tyr Arg Ile Lys Tyr	Pro Lys Ala Asp Met Gln	
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Ile Leu Pro Val Ser Gly Glu Phe Ser	Arg Ala Leu Ala Leu Glu	
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Val Gly Ser Ser Gln Phe Asn Asn Glu	Ser Leu Leu Phe Phe Cys	
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Asp Val Asp Leu Val Phe Thr Thr Glu	Phe Leu Gln Arg Cys Arg	
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Tyr Gly Phe Gly Ile Thr Cys Ile Tyr	Lys Gly Asp Leu Val Arg	
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Arg Ser Gln Glu Val Gly Val Val His	Val His His Pro Val Phe	
740	745	750
Cys Asp Pro Asn Leu Asp Pro Lys Gln	Tyr Lys Met Cys Leu Gly	
755	760	765
Ser Lys Ala Ser Thr Tyr Gly Ser Thr	Gln Gln Leu Ala Glu Met	
770	775	780
Trp Leu Glu Lys Asn Asp Pro Ser Tyr	Ser Lys Ser Ser Asn Asn	
785	790	795
Asn Gly Ser Val Arg Thr Ala		
800		

<210> 261
 <211> 24

<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 261
tgccactac ggggtgtgga cgac 24

<210> 262
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 262
tcccatttct tccgtggtgc ccag 24

<210> 263
<211> 46
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-46
<223> Synthetic construct.

<400> 263
ccagaagaag tccttcatga tgctcaagta catgcacgac cactac 46

<210> 264
<211> 1419
<212> DNA
<213> Homo sapiens

<400> 264
ggacaaccgt tgctgggtgt cccagggct gaggcaggac ggtactccgc 50
tgacacacctc ccttcggcc ttgaggttcc cagcctggtg gccccaggac 100
gttccggtcg catggcagag tgctacggac gacgcctatg aagcccttag 150
tccttctagt tgcgctttg ctatggcctt cgtctgtgcc ggcttatccg 200
agcataactg tgacacactga tgaagagcaa aacttgaatc attatataca 250
agtttttagag aaccttagtac gaagtgttcc ctctggggag ccaggtcgtg 300
agaaaaaaatc taactctcca aaacatgtt attctatagc atcaaaggga 350
tcaaaaattta aggagctagt tacacatgga gacgcttcaa ctgagaatga 400

tgttttaacc aatcctatca gtgaagaaac tacaacttgc cctacaggag 450
gcttcacacc ggaaatagga aagaaaaaac acacggaaag taccccatc 500
tggtcgatca aaccaaacaa tgttccatt gtttgcatt cagaggaacc 550
ttatattgaa aatgaagagc cagagccaga gccggagcca gctgcaaaac 600
aaactgaggc accaagaatg ttgccagttg ttactgaatc atctacaagt 650
ccatatgtta cctcatacaa gtcacctgtc accacttttag ataagagcac 700
tggcatttag atctctacag aatcagaaga tgttcctcag ctctcagggt 750
aaactgcgt agaaaaaccc gaagagttt gaaagcaccc agagagttgg 800
aataatgatg acatttgaa aaaaattttt gatattaatt cacaagtgc 850
acaggcactt ctttgtaca ccagcaaccc agcatataga gaagatattt 900
aagcctctaa agatcaccta aaacgaagcc ttgcctcagc agcagcagca 950
gaacataaat taaaaacaat gtataagtcc cagttattgc cagtaggacg 1000
aacaagtaat aaaatttgatg acatcgaaac tgttattaac atgctgtgta 1050
attctagatc taaactctat gaatatttag atattaaatg tgttccacca 1100
gagatgagag aaaaagctgc tacagtattt aatacattaa aaaatatgtg 1150
tagatcaagg agagtcacag ctttattttt agtttattaa acaataat 1200
aaaaattttt aacctacttg atattccata acaaagctga tttaagcaaa 1250
ctgcattttt tcacaggaga aataatcata ttgcattttt caaaagtgt 1300
ataaaaaatat tttctattgt agttcaaatg tgccaaacatc tttatgtgtc 1350
atgtgttatg aacaattttc atatgcacta aaaacctaatt taaaataaaa 1400
attttggttc aggaaaaaaa 1419

<210> 265

<211> 350

<212> PRT

<213> Homo sapiens

<400> 265

Met	Lys	Pro	Leu	Val	Leu	Leu	Val	Ala	Leu	Leu	Leu	Trp	Pro	Ser
1									10				15	

Ser	Val	Pro	Ala	Tyr	Pro	Ser	Ile	Thr	Val	Thr	Pro	Asp	Glu	Glu
									25				30	

Gln	Asn	Leu	Asn	His	Tyr	Ile	Gln	Val	Leu	Glu	Asn	Leu	Val	Arg
									35				45	

Ser Val Pro Ser Gly Glu Pro Gly Arg Glu Lys Lys Ser Asn Ser

50	55	60
Pro Lys His Val Tyr Ser Ile Ala Ser Lys Gly Ser Lys Phe Lys		
65	70	75
Glu Leu Val Thr His Gly Asp Ala Ser Thr Glu Asn Asp Val Leu		
80	85	90
Thr Asn Pro Ile Ser Glu Glu Thr Thr Thr Phe Pro Thr Gly Gly		
95	100	105
Phe Thr Pro Glu Ile Gly Lys Lys Lys His Thr Glu Ser Thr Pro		
110	115	120
Phe Trp Ser Ile Lys Pro Asn Asn Val Ser Ile Val Leu His Ala		
125	130	135
Glu Glu Pro Tyr Ile Glu Asn Glu Glu Pro Glu Pro Glu Pro Glu		
140	145	150
Pro Ala Ala Lys Gln Thr Glu Ala Pro Arg Met Leu Pro Val Val		
155	160	165
Thr Glu Ser Ser Thr Ser Pro Tyr Val Thr Ser Tyr Lys Ser Pro		
170	175	180
Val Thr Thr Leu Asp Lys Ser Thr Gly Ile Glu Ile Ser Thr Glu		
185	190	195
Ser Glu Asp Val Pro Gln Leu Ser Gly Glu Thr Ala Ile Glu Lys		
200	205	210
Pro Glu Glu Phe Gly Lys His Pro Glu Ser Trp Asn Asn Asp Asp		
215	220	225
Ile Leu Lys Lys Ile Leu Asp Ile Asn Ser Gln Val Gln Gln Ala		
230	235	240
Leu Leu Ser Asp Thr Ser Asn Pro Ala Tyr Arg Glu Asp Ile Glu		
245	250	255
Ala Ser Lys Asp His Leu Lys Arg Ser Leu Ala Leu Ala Ala Ala		
260	265	270
Ala Glu His Lys Leu Lys Thr Met Tyr Lys Ser Gln Leu Leu Pro		
275	280	285
Val Gly Arg Thr Ser Asn Lys Ile Asp Asp Ile Glu Thr Val Ile		
290	295	300
Asn Met Leu Cys Asn Ser Arg Ser Lys Leu Tyr Glu Tyr Leu Asp		
305	310	315
Ile Lys Cys Val Pro Pro Glu Met Arg Glu Lys Ala Ala Thr Val		
320	325	330
Phe Asn Thr Leu Lys Asn Met Cys Arg Ser Arg Arg Val Thr Ala		
335	340	345

Leu Leu Lys Val Tyr
350

<210> 266

<211> 2403

<212> DNA

<213> Homo sapiens

<400> 266

cggtcgagc ggctcgagtg aagagcctct ccacggctcc tgcgcctgag 50
acagctggcc` tgacctccaa atcatccatc caccctgct gtcatctgtt 100
ttcatagtgt gagatcaacc cacaggaata tccatggctt ttgtgctcat 150
tttggttctc agtttctacg agctggtgctc aggacagtgg caagtcactg 200
gaccgggcaa gtttgcctcag gccttgggtgg gggaggacgc cgtgttctcc 250
tgctccctct ttccctgagac cagtgcagag gctatggaag tgcgggttctt 300
caggaatcag ttccatgctg tggccaccc tctacagagat ggggaagact 350
ggaaatctaa gcagatgcca cagtatcgag ggagaactga gtttgcgtt 400
gactccatcg cagggggcg tgtctctcta aggctaaaaa acatcactcc 450
ctcggacatc ggcctgtatg ggtgctgggtt cagttccacg atttacgatg 500
aggaggccac ctgggagctg cgggtggcag cactgggctc acttcctctc 550
atttccatcg tggatatgt tgacggaggt atccagttac tctgcgttgc 600
ctcaggctgg ttcccccagc ccacagccaa gtggaaaggt ccacaaggac 650
aggatttgc ttcagactcc agagcaaatg cagatggta cagcctgtat 700
gatgtggaga tctccattat agtccaggaa aatgctggta gcatattgtg 750
ttccatccac cttgctgagc agagtcatga ggtggaaatcc aaggtattga 800
taggagagac gttttccag ccctcacctt ggcgcctggc ttctattta 850
ctcgggttac tctgtggtgc cctgtgtggt gttgtcatgg ggatgataat 900
tgaaaaatccaaag ggaaaatcca ggcggaaactg gactggagaa 950
gaaagcacgg acaggcagaa ttgagagacg cccggaaaca cgcagtggag 1000
gtgactctgg atccagagac ggctcacccg aagctctgcg tttctgatct 1050
gaaaactgta acccatagaa aagctccccca ggaggtgcct cactctgaga 1100
agagatttac aaggaagagt gtggtggctt ctcagggttt ccaaggcaggg 1150
agacattact gggaggtgga cgtggacaa aatgttagggt ggtatgtggg 1200
agtgtgtcgg gatgacgtag acagggggaa gaacaatgtg actttgtctc 1250

ccaacaatgg gtattgggtc ctcagactga caacagaaca tttgtatttc 1300
acattcaatc cccattttat cagcctcccc cccagcaccc ctcctacacg 1350
agtaggggtc ttccctggact atgagggtgg gaccatctcc ttcttcaata 1400
caaatgacca gtcccttatt tataccctgc tgacatgtca gtttgaaggc 1450
ttgttgagac cctatatcca gcatgcgatg tatgacgagg aaaaggggac 1500
tcccataattc atatgtccag tgtcctgggg atgagacaga gaagaccctg 1550
cttaaaggc cccacaccac agacccagac acagccaagg gagagtgctc 1600
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ttaggttag tttgtaaaaa ctccatccag ctaagcgatc ttgaacaagt 1850
cacaacctcc caggctcctc atttgctagt cacggacagt gattcctgcc 1900
tcacaggtga agattaaaga gacaacgaat gtgaatcatg cttgcaggtt 1950
tgagggcaca gtgttgcta atgatgtgtt tttatattat acattttccc 2000
accataaaact ctgttgctt attccacatt aatttacttt tctctataacc 2050
aaatcaccca tggaaatagtt attgaacacc tgcttgtga ggctcaaaga 2100
ataaaagagga ggtaggattt ttcactgatt ctataagccc agcattacct 2150
gataccaaaa ccaggcaaag aaaacagaag aagaggaagg aaaactacag 2200
gtccatatcc ctcatthaaca cagacacaaa aattctaaat aaaatttaa 2250
caaattaaac taaacaatat atttaaagat gatataaac tactcagtgt 2300
ggtttgtccc acaaatgcag agttggttt atatttaat atcaaccagt 2350
gtaattcagc acattaataa agtaaaaaag aaaaccataa aaaaaaaaaa 2400
aaa 2403

<210> 267
<211> 466
<212> PRT
<213> Homo sapiens

<400> 267
Met Ala Phe Val Leu Ile Leu Val Leu Ser Phe Tyr Glu Leu Val
1 5 10 15
Ser Gly Gln Trp Gln Val Thr Gly Pro Gly Lys Phe Val Gln Ala

20	25	30
Leu Val Gly Glu Asp Ala Val Phe Ser Cys Ser	Leu Phe Pro Glu	
35	40	45
Thr Ser Ala Glu Ala Met Glu Val Arg Phe Phe	Arg Asn Gln Phe	
50	55	60
His Ala Val Val His Leu Tyr Arg Asp Gly Glu	Asp Trp Glu Ser	
65	70	75
Lys Gln Met Pro Gln Tyr Arg Gly Arg ⁹ Thr	Glu Phe Val Lys Asp	
80	85	90
Ser Ile Ala Gly Gly Arg Val Ser Leu Arg	Leu Lys Asn Ile Thr	
95	100	105
Pro Ser Asp Ile Gly Ley Tyr Gly Cys Trp	Phe Ser Ser Gln Ile	
110	115	120
Tyr Asp Glu Glu Ala Thr Trp Glu Leu Arg	Val Ala Ala Leu Gly	
125	130	135
Ser Leu Pro Leu Ile Ser Ile Val Gly Tyr	Val Asp Gly Gly Ile	
140	145	150
Gln Leu Leu Cys Leu Ser Ser Gly Trp	Phe Pro Gln Pro Thr Ala	
155	160	165
Lys Trp Lys Gly Pro Gln Gly Gln Asp	Leu Ser Ser Asp Ser Arg	
170	175	180
Ala Asn Ala Asp Gly Tyr Ser Leu Tyr Asp	Val Glu Ile Ser Ile	
185	190	195
Ile Val Gln Glu Asn Ala Gly Ser Ile	Leu Cys Ser Ile His Leu	
200	205	210
Ala Glu Gln Ser His Glu Val Glu Ser	Lys Val Leu Ile Gly Glu	
215	220	225
Thr Phe Phe Gln Pro Ser Pro Trp Arg	Leu Ala Ser Ile Leu Leu	
230	235	240
Gly Leu Leu Cys Gly Ala Leu Cys Gly	Val Val Met Gly Met Ile	
245	250	255
Ile Val Phe Phe Lys Ser Lys Gly Lys	Ile Gln Ala Glu Leu Asp	
260	265	270
Trp Arg Arg Lys His Gly Gln Ala Glu	Leu Arg Asp Ala Arg Lys	
275	280	285
His Ala Val Glu Val Thr Leu Asp Pro	Glu Thr Ala His Pro Lys	
290	295	300
Leu Cys Val Ser Asp Leu Lys Thr Val	Thr His Arg Lys Ala Pro	
305	310	315

Gln Glu Val Pro His Ser Glu Lys Arg Phe Thr Arg Lys Ser Val
320 325 330
Val Ala Ser Gln Gly Phe Gln Ala Gly Arg His Tyr Trp Glu Val
335 340 345
Asp Val Gly Gln Asn Val Gly Trp Tyr Val Gly Val Cys Arg Asp
350 355 360
Asp Val Asp Arg Gly Lys Asn Asn Val Thr Leu Ser Pro Asn Asn
365 370 375
Gly Tyr Trp Val Leu Arg Leu Thr Thr Glu His Leu Tyr Phe Thr
380 385 390
Phe Asn Pro His Phe Ile Ser Leu Pro Pro Ser Thr Pro Pro Thr
395 400 405
Arg Val Gly Val Phe Leu Asp Tyr Glu Gly Gly Thr Ile Ser Phe
410 415 420
Phe Asn Thr Asn Asp Gln Ser Leu Ile Tyr Thr Leu Leu Thr Cys
425 430 435
Gln Phe Glu Gly Leu Leu Arg Pro Tyr Ile Gln His Ala Met Tyr
440 445 450
Asp Glu Glu Lys Gly Thr Pro Ile Phe Ile Cys Pro Val Ser Trp
455 460 465
Gly

<210> 268
<211> 2103
<212> DNA
<213> Homo sapiens

<400> 268
ccttcacagg acttttcatt gctgggtggc aatgatgtat cggccagatg 50
tggtgagggc tagaaaaaga gtttgggg aaccctgggt tatcggcctc 100
gtcatcttca tatccctgat tgtcctggca gtgtgcattg gactcactgt 150
tcattatgtg agatataatc aaaagaagac ctacaattac tatagcacat 200
tgtcatttac aactgacaaa cttatgctg agttggcag agaggcttct 250
aacaatttta cagaaatgag ccagagactt gaatcaatgg tgaaaaatgc 300
attttataaa tctccattaa gggagaatt tgtcaagtct caggttatca 350
agttcagtca acagaagcat ggagtgttgg ctcatatgct gttgatttgt 400
agatttcact ctactgagga tcctgaaact gtagataaaa ttgttcaact 450
tgttttacat gaaaagctgc aagatgctgt aggacccct aaagtagatc 500

ctcactcagt taaaattaaa aaaatcaaca agacagaaac agacagctat 550
ctaaaccatt gctgcggaac acgaagaagt aaaactctag gtcagagtct 600
caggatcgtt ggtgggacag aagtagaaga gggtaatgg ccctggcagg 650
ctagcctgca gtggatggg agtcatcgct gtggagcaac cttaattaat 700
gccacatggc ttgtgagtgc tgctcactgt tttacaacat ataagaaccc 750
tgccagatgg actgcttcct ttggagtaac aataaaacct tcgaaaatga 800
aacggggctc ccggagaata attgtccatg aaaaatacaa acacccatca 850
catgactatg atatttctct tgcagagctt tctagccctg ttccctacac 900
aatgcagta catagagttt gtctccctga tgcacccatg gagtttcaac 950
caggtgatgt gatgttggc acaggattt gggactgaa aatgtatgg 1000
tacagtcaaa atcatcttcg acaagcacag gtgactctca tagacgctac 1050
aacttgcaat gaacctcaag cttacaatga cgccataact cctagaatgt 1100
tatgtgctgg ctcccttagaa ggaaaaacag atgcatgcca gggtaactct 1150
ggaggaccac tggtagttc agatgctaga gatatctgg accttgctgg 1200
aatagtgagc tggggagatg aatgtgcgaa acccaacaag cctgggtttt 1250
atactagagt tacggcctt cgggactgga ttacttcaaa aactggtatac 1300
taagagacaa aagcctcatg gaacagataa cattttttt tgtttttgg 1350
gtgtggaggc catttttaga gatacagaat tggagaagac ttgcaaaaca 1400
gctagatttgc actgatctca ataaactgtt tgcttgatgc atgtatttc 1450
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tgtcatctgt gagcaatagt taaaacttta tgtacataga gaaatagata 1550
atacaatatt acattacagc ctgtattcat ttgttctcta gaagtttgg 1600
cagaattttg acttggac ataaatttg aatgcataata tacaatttga 1650
agcactcctt ttcttcagtt cctcagctcc tctcatttca gcaaataatcc 1700
atttcaagg tgcagaacaa ggagtgaaag aaaatataag aagaaaaaaa 1750
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aatatttagaa atgatcatat tcattatgaa aggtcaagca aagacagcag 1850
aataccaatc acttcatcat ttaggaagta tggaaactaa gttaaggaag 1900
tccagaaaga agccaagata ttcatttccat ttcatttcca aacaactact 1950

atgataaaatg tgaagaagat tctgttttt tgtgacctat aataattata 2000
caaacttcat gcaatgtact tgttctaagc aaattaaagc aaatatttat 2050
ttaacattgt tactgaggat gtcaacatata aacaataaaa tataaattcac 2100
cca 2103

<210> 269
<211> 423
<212> PRT
<213> Homo sapiens

<400> 269
Met Met Tyr Arg Pro Asp Val Val Arg Ala Arg Lys Arg Val Cys
1 5 10 15
Trp Glu Pro Trp Val Ile Gly Leu Val Ile Phe Ile Ser Leu Ile
20 25 30
Val Leu Ala Val Cys Ile Gly Leu Thr Val His Tyr Val Arg Tyr
35 40 45
Asn Gln Lys Lys Thr Tyr Asn Tyr Tyr Ser Thr Leu Ser Phe Thr
50 55 60
Thr Asp Lys Leu Tyr Ala Glu Phe Gly Arg Glu Ala Ser Asn Asn
65 70 75
Phe Thr Glu Met Ser Gln Arg Leu Glu Ser Met Val Lys Asn Ala
80 85 90
Phe Tyr Lys Ser Pro Leu Arg Glu Glu Phe Val Lys Ser Gln Val
95 100 105
Ile Lys Phe Ser Gln Gln Lys His Gly Val Leu Ala His Met Leu
110 115 120
Leu Ile Cys Arg Phe His Ser Thr Glu Asp Pro Glu Thr Val Asp
125 130 135
Lys Ile Val Gln Leu Val Leu His Glu Lys Leu Gln Asp Ala Val
140 145 150
Gly Pro Pro Lys Val Asp Pro His Ser Val Lys Ile Lys Lys Ile
155 160 165
Asn Lys Thr Glu Thr Asp Ser Tyr Leu Asn His Cys Cys Gly Thr
170 175 180
Arg Arg Ser Lys Thr Leu Gly Gln Ser Leu Arg Ile Val Gly Gly
185 190 195
Thr Glu Val Glu Glu Gly Glu Trp Pro Trp Gln Ala Ser Leu Gln
200 205 210
Trp Asp Gly Ser His Arg Cys Gly Ala Thr Leu Ile Asn Ala Thr
215 220 225

Trp Leu Val Ser Ala Ala His Cys Phe Thr Thr Tyr Lys Asn Pro
 230 235 240
 Ala Arg Trp Thr Ala Ser Phe Gly Val Thr Ile Lys Pro Ser Lys
 245 250 255
 Met Lys Arg Gly Leu Arg Arg Ile Ile Val His Glu Lys Tyr Lys
 260 265 270
 His Pro Ser His Asp Tyr Asp Ile Ser Leu Ala Glu Leu Ser Ser
 275 280 285
 Pro Val Pro Tyr Thr Asn Ala Val His Arg Val Cys Leu Pro Asp
 290 295 300
 Ala Ser Tyr Glu Phe Gln Pro Gly Asp Val Met Phe Val Thr Gly
 305 310 315
 Phe Gly Ala Leu Lys Asn Asp Gly Tyr Ser Gln Asn His Leu Arg
 320 325 330
 Gln Ala Gln Val Thr Leu Ile Asp Ala Thr Thr Cys Asn Glu Pro
 335 340 345
 Gln Ala Tyr Asn Asp Ala Ile Thr Pro Arg Met Leu Cys Ala Gly
 350 355 360
 Ser Leu Glu Gly Lys Thr Asp Ala Cys Gln Gly Asp Ser Gly Gly
 365 370 375
 Pro Leu Val Ser Ser Asp Ala Arg Asp Ile Trp Tyr Leu Ala Gly
 380 385 390
 Ile Val Ser Trp Gly Asp Glu Cys Ala Lys Pro Asn Lys Pro Gly
 395 400 405
 Val Tyr Thr Arg Val Thr Ala Leu Arg Asp Trp Ile Thr Ser Lys
 410 415 420
 Thr Gly Ile

<210> 270

<211> 1170

<212> DNA

<213> Homo sapiens

<400> 270

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cagacgtcag ctgggtggatt cccgctgcat caaggcctac ccactgtctc 150

catgctggc tctccctgcc ttctgtggct cctggccgtg accttcttgg 200

ttcccccagagc tcagcccttg gcccctcaag actttgaaga agaggaggca 250

gatgagactg agacggcgtg gccgccttg ccggctgtcc cctgcgacta 300
cgaccactgc cgacacactgc aggtgccctg caaggagcta cagagggtcg 350
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acttctgcct ggcgatcgc tgggctgcc cgccgcgcgc cgccgcgcga 850
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cctccagggg gggctggacg gcgagctggg agccagcccc aggctccagg 1000
gccacggcgg agtcatggtt ctcaggactg agcgctgtt taggtccggt 1050
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ccccaaatttt ttttaagcg gccagataat aaataatgta acctttgcgg 1150
ttaaaaaaaaaaaaaaaa 1170

<210> 271
<211> 238
<212> PRT
<213> Homo sapiens

<400> 271
Met Leu Gly Ser Pro Cys Leu Leu Trp Leu Leu Ala Val Thr Phe
1 5 10 15
Leu Val Pro Arg Ala Gln Pro Leu Ala Pro Gln Asp Phe Glu Glu
20 25 30
Glu Glu Ala Asp Glu Thr Glu Thr Ala Trp Pro Pro Leu Pro Ala
35 40 45
Val Pro Cys Asp Tyr Asp His Cys Arg His Leu Gln Val Pro Cys
50 55 60
Lys Glu Leu Gln Arg Val Gly Pro Ala Ala Cys Leu Cys Pro Gly
65 70 75

Leu	Ser	Ser	Pro	Ala	Gln	Pro	Pro	Asp	Pro	Pro	Arg	Met	Gly	Glu
80														90
Val	Arg	Ile	Ala	Ala	Glu	Glu	Gly	Arg	Ala	Val	Val	His	Trp	Cys
95														105
Ala	Pro	Phe	Ser	Pro	Val	Leu	His	Tyr	Trp	Leu	Leu	Leu	Trp	Asp
110														120
Gly	Ser	Glu	Ala	Ala	Gln	Lys	Gly	Pro	Pro	Leu	Asn	Ala	Thr	Val
125														135
Arg	Arg	Ala	Glu	Leu	Lys	Gly	Leu	Lys	Pro	Gly	Gly	Ile	Tyr	Val
140														150
Val	Cys	Val	Val	Ala	Ala	Asn	Glu	Ala	Gly	Ala	Ser	Arg	Val	Pro
155														165
Gln	Ala	Gly	Gly	Glu	Gly	Leu	Glu	Gly	Ala	Asp	Ile	Pro	Ala	Phe
170														180
Gly	Pro	Cys	Ser	Arg	Leu	Ala	Val	Pro	Pro	Asn	Pro	Arg	Thr	Leu
185														195
Val	His	Ala	Ala	Val	Gly	Val	Gly	Thr	Ala	Leu	Ala	Leu	Leu	Ser
200														210
Cys	Ala	Ala	Leu	Val	Trp	His	Phe	Cys	Leu	Arg	Asp	Arg	Trp	Gly
215														225
Cys	Pro	Arg	Arg	Ala	Ala	Ala	Arg	Ala	Ala	Gly	Ala	Leu		
230														
235														

<210> 272

<211> 2397

<212> DNA

<213> Homo sapiens

<400> 272

agagaaaagaa gcgtctccag ctgaagccaa tgcagccctc cggctctccg 50

cgaagaagtt ccctgccccg atgagccccc gccgtgcgtc cccgactatc 100

cccaaggcggg cgtggggcac cgggcccagc gccgacgatc gctgccgtt 150

tgccttggg agtaggatgt ggtgaaagga tggggcttct cccttacggg 200

gctcacaatg gccagagaag attccgtgaa gtgtctgcgc tgcctgctct 250

acgccctcaa tctgctctt tggtaatgt ccatcagtgt gttggcagtt 300

tctgcttggg tgagggacta cctaaataat gttctcaatt taactgcaga 350

aacgagggtt gaggaagcag tcattttgac ttacttcct gtggttcatc 400

cggtcatgtat tgctgtttgc tgtttcctta tcattgtggg gatgttagga 450

tattgtggaa cggtgaaaag aaatcttttg cttcttgcatt ggtactttgg 500

aagtttgctt gtcattttct gtgtagaact ggcttgtggc gtttggacat 550
atgaacagga acttatggtt ccagtacaat ggtcagatat ggtcactttg 600
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cagaaatatg tagaaataaa aatgttgcca taaaataaca cctaagcata 1250
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<210> 273

<211> 305

<212> PRT

<213> Homo sapiens

<400> 273

Met Ala Arg Glu Asp Ser Val Lys Cys Leu Arg Cys Leu Leu Tyr
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Ala Leu Asn Leu Leu Phe Trp Leu Met Ser Ile Ser Val Leu Ala
20 25 30

Val Ser Ala Trp Met Arg Asp Tyr Leu Asn Asn Val Leu Thr Leu
35 40 45

Thr Ala Glu Thr Arg Val Glu Glu Ala Val Ile Leu Thr Tyr Phe
50 55 60

Pro Val Val His Pro Val Met Ile Ala Val Cys Cys Phe Leu Ile
65 70 75

Ile Val Gly Met Leu Gly Tyr Cys Gly Thr Val Lys Arg Asn Leu
80 85 90

Leu Leu Leu Ala Trp Tyr Phe Gly Ser Leu Leu Val Ile Phe Cys
95 100 105

Val Glu Leu Ala Cys Gly Val Trp Thr Tyr Glu Gln Glu Leu Met
110 115 120

Val Pro Val Gln Trp Ser Asp Met Val Thr Leu Lys Ala Arg Met
125 130 135

Thr Asn Tyr Gly Leu Pro Arg Tyr Arg Trp Leu Thr His Ala Trp
140 145 150

Asn Phe Phe Gln Arg Glu Phe Lys Cys Cys Gly Val Val Tyr Phe
155 160 165

Thr Asp Trp Leu Glu Met Thr Glu Met Asp Trp Pro Pro Asp Ser

170	175	180
Cys Cys Val Arg Glu Phe Pro Gly Cys	Ser Lys Gln Ala His Gln	
185	190	195
Glu Asp Leu Ser Asp Leu Tyr Gln Glu	Gly Cys Gly Lys Lys	Met
200	205	210
Tyr Ser Phe Leu Arg Gly Thr Lys Gln	Leu Gln Val Leu Arg	Phe
215	220	225
Leu Gly Ile Ser Ile Gly Val Thr Gln	Ile Leu Ala Met Ile	Leu
230	235	240
Thr Ile Thr Leu Leu Trp Ala Leu Tyr	Tyr Asp Arg Arg	Glu Pro
245	250	255
Gly Thr Asp Gln Met Met Ser Leu Lys	Asn Asp Asn Ser Gln	His
260	265	270
Leu Ser Cys Pro Ser Val Glu Leu Leu	Lys Pro Ser Leu Ser	Arg
275	280	285
Ile Phe Glu His Thr Ser Met Ala Asn	Ser Phe Asn Thr His	Phe
290	295	300
Glu Met Glu Glu Leu		
305		

<210> 274

<211> 2063

<212> DNA

<213> Homo sapiens

<400> 274

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ttctgacctg ctggccagcc aggacctgtg tggggaggcc ctccctgctgc 150

cttggggta caatctcagc tccaggctac agggaga^ccg ggaggatcac 200

agagccagca ttttacagga tcctgacagt gatcaacctc tgaacagcct 250

cgatgtcaaa cccctgcgca aaccccgat ccccatggag accttcagaa 300

aggtggggat ccccatcatc atagcaactac tgaggctggc gagtatcatc 350

attgtggttg tcctcatcaa ggtgattctg gataaatact acttcctctg 400

cgggcagcct ctccacttca tccccgagaa gcagctgtgt gacggagagc 450

tggactgtcc cttgggggag gacgaggagc actgtgtcaa gagcttcccc 500

gaagggcctg cagtggcagt ccgcctctcc aaggaccgat ccacactgca 550

ggtgctggac tcggccacag ggaactggtt ctctgcctgt ttgcacaact 600

tcacagaagc tctcgctgag acagcctgta ggcagatggg ctacagcaga 650
gctgtggaga ttggcccaaga ccaggatctg gatgttggta aaatcacaga 700
aaacagccag gagttcgca tgcggaaactc aagtggccc tgtctctcag 750
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aatgcactgc cctactgttg gtatgactac cgttacctac tgggttcatt 2000
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caaaaaaaaaaaa aaa 2063

<210> 275

<211> 432

<212> PRT

<213> Homo sapiens

<400> 275

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Val	Lys	Pro	Leu	Arg	Lys	Pro	Arg	Ile	Pro	Met	Glu	Thr	Phe	Arg
	20							25						30
Lys	Val	Gly	Ile	Pro	Ile	Ile	Ile	Ala	Leu	Leu	Ser	Leu	Ala	Ser
	35							40						45
Ile	Ile	Ile	Val	Val	Val	Leu	Ile	Lys	Val	Ile	Leu	Asp	Lys	Tyr
	50							55						60
Tyr	Phe	Leu	Cys	Gly	Gln	Pro	Leu	His	Phe	Ile	Pro	Arg	Lys	Gln
	65							70						75
Leu	Cys	Asp	Gly	Glu	Leu	Asp	Cys	Pro	Leu	Gly	Glu	Asp	Glu	Glu
	80							85						90
His	Cys	Val	Lys	Ser	Phe	Pro	Glu	Gly	Pro	Ala	Val	Ala	Val	Arg
	95							100						105
Leu	Ser	Lys	Asp	Arg	Ser	Thr	Leu	Gln	Val	Leu	Asp	Ser	Ala	Thr
	110							115						120
Gly	Asn	Trp	Phe	Ser	Ala	Cys	Phe	Asp	Asn	Phe	Thr	Glu	Ala	Leu
	125							130						135
Ala	Glu	Thr	Ala	Cys	Arg	Gln	Met	Gly	Tyr	Ser	Arg	Ala	Val	Glu
	140							145						150
Ile	Gly	Pro	Asp	Gln	Asp	Leu	Asp	Val	Val	Glu	Ile	Thr	Glu	Asn
	155							160						165
Ser	Gln	Glu	Leu	Arg	Met	Arg	Asn	Ser	Ser	Gly	Pro	Cys	Leu	Ser
	170							175						180
Gly	Ser	Leu	Val	Ser	Leu	His	Cys	Leu	Ala	Cys	Gly	Lys	Ser	Leu
	185							190						195
Lys	Thr	Pro	Arg	Val	Val	Gly	Gly	Glu	Ala	Ser	Val	Asp	Ser	
	200							205						210
Trp	Pro	Trp	Gln	Val	Ser	Ile	Gln	Tyr	Asp	Lys	Gln	His	Val	Cys
	215							220						225
Gly	Gly	Ser	Ile	Leu	Asp	Pro	His	Trp	Val	Leu	Thr	Ala	Ala	His
	230							235						240
Cys	Phe	Arg	Lys	His	Thr	Asp	Val	Phe	Asn	Trp	Lys	Val	Arg	Ala
	245							250						255

Gly Ser Asp Lys Leu Gly Ser Phe Pro Ser Leu Ala Val Ala Lys
 260 265 270
 Ile Ile Ile Ile Glu Phe Asn Pro Met Tyr Pro Lys Asp Asn Asp
 275 280 285
 Ile Ala Leu Met Lys Leu Gln Phe Pro Leu Thr Phe Ser Gly Thr
 290 295 300
 Val Arg Pro Ile Cys Leu Pro Phe Phe Asp Glu Glu Leu Thr Pro
 305 310 315
 Ala Thr Pro Leu Trp Ile Ile Gly Trp Gly Phe Thr Lys Gln Asn
 320 325 330
 Gly Gly Lys Met Ser Asp Ile Leu Leu Gln Ala Ser Val Gln Val
 335 340 345
 Ile Asp Ser Thr Arg Cys Asn Ala Asp Asp Ala Tyr Gln Gly Glu
 350 355 360
 Val Thr Glu Lys Met Met Cys Ala Gly Ile Pro Glu Gly Gly Val
 365 370 375
 Asp Thr Cys Gln Gly Asp Ser Gly Gly Pro Leu Met Tyr Gln Ser
 380 385 390
 Asp Gln Trp His Val Val Gly Ile Val Ser Trp Gly Tyr Gly Cys
 395 400 405
 Gly Gly Pro Ser Thr Pro Gly Val Tyr Thr Lys Val Ser Ala Tyr
 410 415 420
 Leu Asn Trp Ile Tyr Asn Val Trp Lys Ala Glu Leu
 425 430

<210> 276
 <211> 3143
 <212> DNA
 <213> Homo sapiens

<400> 276
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 ttttcctctt ccaactgctt cagctgctgc tgccgacgac gaccgcgggg 200
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 ctctgctcct gagtggtgat ggaaatactc tctacgtggg ggctcgagaa 350
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catgataccg tggccagcca gtgacagaaaa aaagagtcaa tgcgccttta 450
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agagactgtt tatttttat taaaaatata aggttaaaa aaa 3143

<210> 277
<211> 761
<212> PRT
<213> Homo sapiens

<400> 277

Met Ala Leu Pro Ala Leu Gly Leu Asp Pro Trp Ser Leu Leu Gly
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Leu Phe Leu Phe Gln Leu Leu Gln Leu Leu Leu Pro Thr Thr Thr
 20 25 30

Ala Gly Gly Gly Gln Gly Pro Met Pro Arg Val Arg Tyr Tyr
 35 40 45

Ala Gly Asp Glu Arg Arg Ala Leu Ser Phe Phe His Gln Lys Gly
 50 55 60

Leu Gln Asp Phe Asp Thr Leu Leu Leu Ser Gly Asp Gly Asn Thr
 65 70 75

Leu Tyr Val Gly Ala Arg Glu Ala Ile Leu Ala Leu Asp Ile Gln
 80 85 90

Asp Pro Gly Val Pro Arg Leu Lys Asn Met Ile Pro Trp Pro Ala
 95 100 105

Ser Asp Arg Lys Lys Ser Glu Cys Ala Phe Lys Lys Lys Ser Asn
 110 115 120

Glu Thr Gln Cys Phe Asn Phe Ile Arg Val Leu Val Ser Tyr Asn
 125 130 135

Val Thr His Leu Tyr Thr Cys Gly Thr Phe Ala Phe Ser Pro Ala
 140 145 150

Cys Thr Phe Ile Glu Leu Gln Asp Ser Tyr Leu Leu Pro Ile Ser
 155 160 165

Glu Asp Lys Val Met Glu Gly Lys Gly Gln Ser Pro Phe Asp Pro
 170 175 180

Ala His Lys His Thr Ala Val Leu Val Asp Gly Met Leu Tyr Ser
 185 190 195

Gly Thr Met Asn Asn Phe Leu Gly Ser Glu Pro Ile Leu Met Arg
 200 205 210

Thr Leu Gly Ser Gln Pro Val Leu Lys Thr Asp Asn Phe Leu Arg
 215 220 225

Trp Leu His His Asp Ala Ser Phe Val Ala Ala Ile Pro Ser Thr
 230 235 240

Gln Val Val Tyr Phe Phe Phe Glu Glu Thr Ala Ser Glu Phe Asp
 245 250 255

Phe Phe Glu Arg Leu His Thr Ser Arg Val Ala Arg Val Cys Lys
 260 265 270

Asn Asp Val Gly Gly Glu Lys Leu Leu Gln Lys Lys Trp Thr Thr
 275 280 285

Phe Leu Lys Ala Gln Leu Leu Cys Thr Gln Pro Gly Gln Leu Pro

290	295	300
Phe Asn Val Ile Arg His Ala Val Leu	Leu Pro Ala Asp Ser	Pro
305	310	315
Thr Ala Pro His Ile Tyr Ala Val Phe	Thr Ser Gln Trp Gln Val	
320	325	330
Gly Gly Thr Arg Ser Ser Ala Val Cys	Ala Phe Ser Leu Leu Asp	
335	340	345
Ile Glu Arg Val Phe Lys Gly Lys Tyr	Lys Glu Leu Asn Lys Glu	
350	355	360
Thr Ser Arg Trp Thr Thr Tyr Arg Gly	Pro Glu Thr Asn Pro Arg	
365	370	375
Pro Gly Ser Cys Ser Val Gly Pro Ser	Ser Asp Lys Ala Leu Thr	
380	385	390
Phe Met Lys Asp His Phe Leu Met Asp	Glu Gln Val Val Gly Thr	
395	400	405
Pro Leu Leu Val Lys Ser Gly Val Glu	Tyr Thr Arg Leu Ala Val	
410	415	420
Glu Thr Ala Gln Gly Leu Asp Gly His	Ser His Leu Val Met Tyr	
425	430	435
Leu Gly Thr Thr Gly Ser Leu His	Lys Ala Val Val Ser Gly	
440	445	450
Asp Ser Ser Ala His Leu Val Glu Glu	Ile Gln Leu Phe Pro Asp	
455	460	465
Pro Glu Pro Val Arg Asn Leu Gln Leu	Ala Pro Thr Gln Gly Ala	
470	475	480
Val Phe Val Gly Phe Ser Gly Val	Trp Arg Val Pro Arg Ala	
485	490	495
Asn Cys Ser Val Tyr Glu Ser Cys Val	Asp Cys Val Leu Ala Arg	
500	505	510
Asp Pro His Cys Ala Trp Asp Pro Glu	Ser Arg Thr Cys Cys Leu	
515	520	525
Leu Ser Ala Pro Asn Leu Asn Ser Trp	Lys Gln Asp Met Glu Arg	
530	535	540
Gly Asn Pro Glu Trp Ala Cys Ala Ser	Gly Pro Met Ser Arg Ser	
545	550	555
Leu Arg Pro Gln Ser Arg Pro Gln Ile	Ile Lys Glu Val Leu Ala	
560	565	570
Val Pro Asn Ser Ile Leu Glu Leu Pro	Cys Pro His Leu Ser Ala	
575	580	585

Leu Ala Ser Tyr Tyr Trp Ser His Gly Pro Ala Ala Val Pro Glu
590 595 600
Ala Ser Ser Thr Val Tyr Asn Gly Ser Leu Leu Leu Ile Val Gln
605 610 615
Asp Gly Val Gly Gly Leu Tyr Gln Cys Trp Ala Thr Glu Asn Gly
620 625 630
Phe Ser Tyr Pro Val Ile Ser Tyr Trp Val Asp Ser Gln Asp Gln
635 640 645
Thr Leu Ala Leu Asp Pro Glu Leu Ala Gly Ile Pro Arg Glu His
650 655 660
Val Lys Val Pro Leu Thr Arg Val Ser Gly Gly Ala Ala Leu Ala
665 670 675
Ala Gln Gln Ser Tyr Trp Pro His Phe Val Thr Val Thr Val Leu
680 685 690
Phe Ala Leu Val Leu Ser Gly Ala Leu Ile Ile Leu Val Ala Ser
695 700 705
Pro Leu Arg Ala Leu Arg Ala Arg Gly Lys Val Gln Gly Cys Glu
710 715 720
Thr Leu Arg Pro Gly Glu Lys Ala Pro Leu Ser Arg Glu Gln His
725 730 735
Leu Gln Ser Pro Lys Glu Cys Arg Thr Ser Ala Ser Asp Val Asp
740 745 750
Ala Asp Asn Asn Cys Leu Gly Thr Glu Val Ala
755 760

<210> 278

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 278

ctgctggta aatctggcgt ggag 24

<210> 279

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 279
gtctggtcct ggctgtccac ccag 24

<210> 280
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 280
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<210> 281
<211> 2320
<212> DNA
<213> Homo sapiens

<400> 281
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atctacagta ggtgaaagcc attatctact gatggaccgg gtttctcaga 200
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ccttttatgc cagatttaa aaaggaagaa aaatcatatc aagttatcag 300
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tctttctgga agaaacttta ggtggcagag gaaaatttga aaacttatta 400
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ggatatcatg gattccttaa agaatgagaa ctgcacatg gtgatagttg 500
aaactttga ctactgtcct ttcctgattt ctgagaagct tgggaagcca 550
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<210> 282
<211> 523
<212> PRT
<213> Homo sapiens

<400> 282
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1 5 10 15
Gly Val Leu Leu Ser Glu Ala Ala Lys Ile Leu Thr Ile Ser Thr
20 25 30
Val Gly Gly Ser His Tyr Leu Leu Met Asp Arg Val Ser Gln Ile
35 40 45
Leu Gln Asp His Gly His Asn Val Thr Met Leu Asn His Lys Arg
50 55 60
Gly Pro Phe Met Pro Asp Phe Lys Lys Glu Glu Lys Ser Tyr Gln
65 70 75
Val Ile Ser Trp Leu Ala Pro Glu Asp His Gln Arg Glu Phe Lys
80 85 90
Lys Ser Phe Asp Phe Phe Leu Glu Glu Thr Leu Gly Gly Arg Gly
95 100 105
Lys Phe Glu Asn Leu Leu Asn Val Leu Glu Tyr Leu Ala Leu Gln
110 115 120
Cys Ser His Phe Leu Asn Arg Lys Asp Ile Met Asp Ser Leu Lys
125 130 135
Asn Glu Asn Phe Asp Met Val Ile Val Glu Thr Phe Asp Tyr Cys
140 145 150
Pro Phe Leu Ile Ala Glu Lys Leu Gly Lys Pro Phe Val Ala Ile
155 160 165
Leu Ser Thr Ser Phe Gly Ser Leu Glu Phe Gly Leu Pro Ile Pro
170 175 180
Leu Ser Tyr Val Pro Val Phe Arg Ser Leu Leu Thr Asp His Met
185 190 195
Asp Phe Trp Gly Arg Val Lys Asn Phe Leu Met Phe Phe Ser Phe
200 205 210
Cys Arg Arg Gln Gln His Met Gln Ser Thr Phe Asp Asn Thr Ile
215 220 225
Lys Glu His Phe Thr Glu Gly Ser Arg Pro Val Leu Ser His Leu
230 235 240
Leu Leu Lys Ala Glu Leu Trp Phe Ile Asn Ser Asp Phe Ala Phe
245 250 255
Asp Phe Ala Arg Pro Leu Leu Pro Asn Thr Val Tyr Val Gly Gly

260	265	270
Leu Met Glu Lys Pro Ile Lys Pro Val Pro Gln Asp Leu Glu Asn		
275	280	285
Phe Ile Ala Lys Phe Gly Asp Ser Gly Phe Val Leu Val Thr Leu		
290	295	300
Gly Ser Met Val Asn Thr Cys Gln Asn Pro Glu Ile Phe Lys Glu		
305	310	315
Met Asn Asn Ala Phe Ala His Leu Pro Gln Gly Val Ile Trp Lys		
320	325	330
Cys Gln Cys Ser His Trp Pro Lys Asp Val His Leu Ala Ala Asn		
335	340	345
Val Lys Ile Val Asp Trp Leu Pro Gln Ser Asp Leu Leu Ala His		
350	355	360
Pro Ser Ile Arg Leu Phe Val Thr His Gly Gly Gln Asn Ser Ile		
365	370	375
Met Glu Ala Ile Gln His Gly Val Pro Met Val Gly Ile Pro Leu		
380	385	390
Phe Gly Asp Gln Pro Glu Asn Met Val Arg Val Glu Ala Lys Lys		
395	400	405
Phe Gly Val Ser Ile Gln Leu Lys Lys Leu Lys Ala Glu Thr Leu		
410	415	420
Ala Leu Lys Met Lys Gln Ile Met Glu Asp Lys Arg Tyr Lys Ser		
425	430	435
Ala Ala Val Ala Ala Ser Val Ile Leu Arg Ser His Pro Leu Ser		
440	445	450
Pro Thr Gln Arg Leu Val Gly Trp Ile Asp His Val Leu Gln Thr		
455	460	465
Gly Gly Ala Thr His Leu Lys Pro Tyr Val Phe Gln Gln Pro Trp		
470	475	480
His Glu Gln Tyr Leu Phe Asp Val Phe Val Phe Leu Leu Gly Leu		
485	490	495
Thr Leu Gly Thr Leu Trp Leu Cys Gly Lys Leu Leu Gly Met Ala		
500	505	510
Val Trp Trp Leu Arg Gly Ala Arg Lys Val Lys Glu Thr		
515	520	

<210> 283
 <211> 24
 <212> DNA
 <213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 283
tgcctttgct cacctacccc aagg 24

<210> 284
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 284
tcaggcttgtt ctccaaagag aggg 24

<210> 285
<211> 45
<212> DNA
<213> Artificial

<220>
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<222> 1-45
<223> Synthetic construct.

<400> 285
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<210> 286
<211> 2340
<212> DNA
<213> Homo sapiens

<400> 286
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gtgctgtccc atccagcagg gctaccctga agctctggct gcagccctcc 200
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<210> 287

<211> 205

<212> PRT

<213> Homo sapiens

<400> 287

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Pro	Gly	Leu	Pro	Leu	Val	Leu	Val	Leu	Leu	Ala	Leu	Gly	Ala	Gly
		20						25						30
Trp	Ala	Gln	Glu	Gly	Ser	Glu	Pro	Val	Leu	Leu	Glu	Gly	Glu	Cys
		35						40						45
Leu	Val	Val	Cys	Glu	Pro	Gly	Arg	Ala	Ala	Ala	Gly	Gly	Pro	Gly
		50						55						60
Gly	Ala	Ala	Leu	Gly	Glu	Ala	Pro	Pro	Gly	Arg	Val	Ala	Phe	Ala
		65						70						75
Ala	Val	Arg	Ser	His	His	His	Glu	Pro	Ala	Gly	Glu	Thr	Gly	Asn
		80						85						90
Gly	Thr	Ser	Gly	Ala	Ile	Tyr	Phe	Asp	Gln	Val	Leu	Val	Asn	Glu
		95						100						105
Gly	Gly	Gly	Phe	Asp	Arg	Ala	Ser	Gly	Ser	Phe	Val	Ala	Pro	Val
		110							115					120
Arg	Gly	Val	Tyr	Ser	Phe	Arg	Phe	His	Val	Val	Lys	Val	Tyr	Asn
		125							130					135
Arg	Gln	Thr	Val	Gln	Val	Ser	Leu	Met	Leu	Asn	Thr	Trp	Pro	Val
		140							145					150
Ile	Ser	Ala	Phe	Ala	Asn	Asp	Pro	Asp	Val	Thr	Arg	Glu	Ala	Ala
		155							160					165
Thr	Ser	Ser	Val	Leu	Leu	Pro	Leu	Asp	Pro	Gly	Asp	Arg	Val	Ser

170 175 180
Leu Arg Leu Arg Arg Gly Asn Leu Leu Gly Gly Trp Lys Tyr Ser
185 190 195
Ser Phe Ser Gly Phe Leu Ile Phe Pro Leu
200 205

<210> 288
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 288
aggcagccac cagctctgtg ctac 24

<210> 289
<211> 27
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-27
<223> Synthetic construct.

<400> 289
cagagaggg a agatgaggaa gccagag 27

<210> 290
<211> 42
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-42
<223> Synthetic construct.

<400> 290
ctgtgctact gcccttggac cctggggacc gagtgtctc gc 42

<210> 291
<211> 1570
<212> DNA
<213> Homo sapiens

<400> 291
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aaaaaaaaaa aaaaaaaaaa 1570

<210> 292
<211> 388
<212> PRT
<213> Homo sapiens

<400> 292

Met	Lys	Thr	Leu	Ile	Ala	Ala	Tyr	Ser	Gly	Val	Leu	Arg	Gly	Glu
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Arg	Gln	Ala	Glu	Ala	Asp	Arg	Ser	Gln	Arg	Ser	His	Gly	Gly	Pro
			20						25					30
Ala	Leu	Ser	Arg	Glu	Gly	Ser	Gly	Arg	Trp	Gly	Thr	Gly	Ser	Ser
			35						40					45
Ile	Leu	Ser	Ala	Leu	Gln	Asp	Leu	Phe	Ser	Val	Thr	Trp	Leu	Asn
				50					55					60
Arg	Ser	Lys	Val	Glu	Lys	Gln	Leu	Gln	Val	Ile	Ser	Val	Leu	Gln
			65						70					75
Trp	Val	Leu	Ser	Phe	Leu	Val	Leu	Gly	Val	Ala	Cys	Ser	Ala	Ile
				80					85					90
Leu	Met	Tyr	Ile	Phe	Cys	Thr	Asp	Cys	Trp	Leu	Ile	Ala	Val	Leu
				95					100					105
Tyr	Phe	Thr	Trp	Leu	Val	Phe	Asp	Trp	Asn	Thr	Pro	Lys	Gly	
				110					115					120
Gly	Arg	Arg	Ser	Gln	Trp	Val	Arg	Asn	Trp	Ala	Val	Trp	Arg	Tyr
				125					130					135
Phe	Arg	Asp	Tyr	Phe	Pro	Ile	Gln	Leu	Val	Lys	Thr	His	Asn	Leu
				140					145					150
Leu	Thr	Thr	Arg	Asn	Tyr	Ile	Phe	Gly	Tyr	His	Pro	His	Gly	Ile
				155					160					165
Met	Gly	Leu	Gly	Ala	Phe	Cys	Asn	Phe	Ser	Thr	Glu	Ala	Thr	Glu
				170					175					180
Val	Ser	Lys	Lys	Phe	Pro	Gly	Ile	Arg	Pro	Tyr	Leu	Ala	Thr	Leu
				185					190					195
Ala	Gly	Asn	Phe	Arg	Met	Pro	Val	Leu	Arg	Glu	Tyr	Leu	Met	Ser
				200					205					210
Gly	Gly	Ile	Cys	Pro	Val	Ser	Arg	Asp	Thr	Ile	Asp	Tyr	Leu	Leu
				215					220					225
Ser	Lys	Asn	Gly	Ser	Gly	Asn	Ala	Ile	Ile	Ile	Val	Val	Gly	Gly
				230					235					240
Ala	Ala	Glu	Ser	Leu	Ser	Ser	Met	Pro	Gly	Lys	Asn	Ala	Val	Thr
				245					250					255
Leu	Arg	Asn	Arg	Lys	Gly	Phe	Val	Lys	Leu	Ala	Leu	Arg	His	Gly

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Ala Asp Leu Val Pro Ile Tyr Ser Phe	Gly Glu Asn Glu Val Tyr	
275	280	285
Lys Gln Val Ile Phe Glu Glu Gly Ser	Trp Gly Arg Trp Val Gln	
290	295	300
Lys Lys Phe Gln Lys Tyr Ile Gly Phe	Ala Pro Cys Ile Phe His	
305	310	315
Gly Arg Gly Leu Phe Ser Ser Asp Thr	Trp Gly Leu Val Pro Tyr	
320	325	330
Ser Lys Pro Ile Thr Thr Val Val Gly	Glu Pro Ile Thr Ile Pro	
335	340	345
Lys Leu Glu His Pro Thr Gln Gln Asp	Ile Asp Leu Tyr His Thr	
350	355	360
Met Tyr Met Glu Ala Leu Val Lys Leu	Phe Asp Lys His Lys Thr	
365	370	375
Lys Phe Gly Leu Pro Glu Thr Glu Val	Leu Glu Val Asn	
380	385	

<210> 293
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 293
 gctgacacctgg ttcccatctta ctcc 24

<210> 294
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 294
 cccacagaca cccatgacac ttcc 24

<210> 295
 <211> 50
 <212> DNA
 <213> Artificial

<220>

<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 295
aagaatgaat tgtacaaagc aggtgatctt cgaggagggc tcctggggcc 50

<210> 296
<211> 3060
<212> DNA
<213> Homo sapiens

<400> 296
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cagaaatcat gggagccagg agatagtggg atgaacactg ttgaaggcaa 1950
aaccttcaac tctaatttggacttttga gtcttagatg gtcctgac 2000
cttgcattc agggacagtt ttcaatttta atccctaata acaatttgc 2050
aagcttccctt gacctgtagg aaggcctgtc tttaggcccgg gcacagtggc 2100
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ggggtcaggc tgatctcaaa ctcctgatc caggtgatct gcccgcctca 2200
gcctccaaa gtgttgcgtat tgcaggcgtg agccactgct cctggccgg 2250
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ccaggggagac tgaagtggga ggatcgctt ggcattgagaa gtcgaggctg 3000
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accctgtctc 3060

<210> 297

<211> 368

<212> PRT

<213> Homo sapiens

<400> 297

Met Gly Leu Leu Ala Phe Leu Lys Thr Gln Phe Val Leu His Leu
1 5 10 15

Leu Val Gly Phe Val Phe Val Val Ser Gly Leu Val Ile Asn Phe
20 25 30

Val Gln Leu Cys Thr Leu Ala Leu Trp Pro Val Ser Lys Gln Leu
35 40 45

Tyr Arg Arg Leu Asn Cys Arg Leu Ala Tyr Ser Leu Trp Ser Gln
50 55 60

Leu Val Met Leu Leu Glu Trp Trp Ser Cys Thr Glu Cys Thr Leu
65 70 75

Phe Thr Asp Gln Ala Thr Val Glu Arg Phe Gly Lys Glu His Ala
80 85 90

Val Ile Ile Leu Asn His Asn Phe Glu Ile Asp Phe Leu Cys Gly
95 100 105

Trp Thr Met Cys Glu Arg Phe Gly Val Leu Gly Ser Ser Lys Val
110 115 120

Leu Ala Lys Lys Glu Leu Leu Tyr Val Pro Leu Ile Gly Trp Thr
125 130 135

Trp Tyr Phe Leu Glu Ile Val Phe Cys Lys Arg Lys Trp Glu Glu
140 145 150

Asp Arg Asp Thr Val Val Glu Gly Leu Arg Arg Leu Ser Asp Tyr
155 160 165

Pro Glu Tyr Met Trp Phe Leu Leu Tyr Cys Glu Gly Thr Arg Phe
 170 175 180
 Thr Glu Thr Lys His Arg Val Ser Met Glu Val Ala Ala Ala Lys
 185 190 195
 Gly Leu Pro Val Leu Lys Tyr His Leu Leu Pro Arg Thr Lys Gly
 200 205 210
 Phe Thr Thr Ala Val Lys Cys Leu Arg Gly Thr Val Ala Ala Val
 215 220 225
 Tyr Asp Val Thr Leu Asn Phe Arg Gly Asn Lys Asn Pro Ser Leu
 230 235 240
 Leu Gly Ile Leu Tyr Gly Lys Lys Tyr Glu Ala Asp Met Cys Val
 245 250 255
 Arg Arg Phe Pro Leu Glu Asp Ile Pro Leu Asp Glu Lys Glu Ala
 260 265 270
 Ala Gln Trp Leu His Lys Leu Tyr Gln Glu Lys Asp Ala Leu Gln
 275 280 285
 Glu Ile Tyr Asn Gln Lys Gly Met Phe Pro Gly Glu Gln Phe Lys
 290 295 300
 Pro Ala Arg Arg Pro Trp Thr Leu Leu Asn Phe Leu Ser Trp Ala
 305 310 315
 Thr Ile Leu Leu Ser Pro Leu Phe Ser Phe Val Leu Gly Val Phe
 320 325 330
 Ala Ser Gly Ser Pro Leu Leu Ile Leu Thr Phe Leu Gly Phe Val
 335 340 345
 Gly Ala Ala Ser Phe Gly Val Arg Arg Leu Ile Gly Glu Ser Leu
 350 355 360
 Glu Pro Gly Arg Trp Arg Leu Gln
 365

<210> 298

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 298

cttcctctgt gggtggacca tgtg 24

<210> 299

<211> 21

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-21

<223> Synthetic construct.

<400> 299
gccacacctcca tgctaacgcg g 21

<210> 300

<211> 45

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-45

<223> Synthetic construct.

<400> 300
ccaaggtcct cgctaagaag gagctgctct acgtccccct catcg 45

<210> 301

<211> 1334

<212> DNA

<213> Homo sapiens

<400> 301
gatattcttt attttaaga atctgaagta ctatgcata ctcctccaa 50
tgtcctgggg cagccaccag gcatattcat ctttgtgtgt gttttcttt 100
tgcttttagca ctggggcact tcttgcttat ttctttggta ggaaaggggc 150
tcagtttgc ttgtggggtt ggtggcaggc aggccggctt acgcctgata 200
cggccctggg ttagaaggga agggaagata aactttata caaatgggga 250
tagctggggt ctgagacctg cttcctcagt aaaattcctg ggatctgcct 300
ataccttctt ttctctaacc tggcataaccc tgcttaaägc ctctcagggc 350
ttctctctgt tcttaggatc aaagtattta gagctacaag agccctcatg 400
gtctggcccc tgccccccctg gccagctca ttgtacatgt ggtgttctct 450
tgtcgttcct gtaatgtggt atgccatggg gtcttgcac aagccttcc 500
tctttggctg gacactgttc cctgcccccc ccatactctt cctacttaat 550
atgttagtcat cctgcagatt tcaattctaa catcatttc tccagggatc 600
ctggcctgac agaatctcat cttgtttaat gctctcataa gaccacttgt 650
ttccctttg cagcacttgc cactcagttg tatctttatg tgcgtttgtg 700
gttgtatggg ttgtgtctgt tccccagaat gcccagctct gagctgcgtg 750

agggtcaagg gcattgctgt gcctgccagg tatagtgcct acatgtggtg 800
ggtgctcatg ttttagagac taaatggagg aggagatgag gaaaagattg 850
aaatctctca gttcaccaga tggtgttaggg cccagcattg taaattcaca 900
cggtgactgt gcttgtaat tatctgggg tgcaggtcct gattcagtag 950
gcccaggttggc catgtatccc acgtgatgct gatgctggc 1000
ctatgaacta tactaaatag taagaatcta tggagccagg ctgggcatgg 1050
tggctcacac ctatgatccc agcactttgg gaggctgagg caggctgatc 1100
acctggagtc aggatttcaa gactagcctg gccaacatgg tggaaacccca 1150
tctgtactaa aaatacacaa attagctggg catggtgca catgcctgta 1200
gtccccagcttggc tggggaggc tgaagcaaga gaatcgcttgg aacctgggag 1250
gcggaggttggc cagtgagccg agatcaggcc actgtattcc aaccagggtg 1300
acagagttagtgc actctatgtc caaaaaaaaaaaa aaaa 1334

<210> 302

<211> 143

<212> PRT

<213> Homo sapiens

<400> 302

Met	His	His	Ser	Leu	Gln	Cys	Pro	Gly	Ala	Ala	Thr	Arg	His	Ile
1				5					10				15	
His	Leu	Cys	Val	Cys	Phe	Ser	Phe	Ala	Leu	Ala	Leu	Gly	His	Phe
			20						25				30	
Leu	Leu	Ile	Ser	Leu	Val	Gly	Lys	Gly	Leu	Ser	Leu	Ser	Cys	Gly
				35					40				45	
Val	Gly	Gly	Arg	Gln	Ala	Gly	Leu	Arg	Leu	Ile	Arg	Pro	Trp	Val
				50					55				60	
Arg	Arg	Glu	Gly	Lys	Ile	Asn	Phe	Tyr	Thr	Asn	Gly	Asp	Ser	Trp
				65					70				75	
Gly	Leu	Arg	Pro	Ala	Ser	Ser	Val	Lys	Phe	Leu	Gly	Ser	Ala	Tyr
				80					85				90	
Thr	Phe	Phe	Ser	Leu	Thr	Trp	His	Thr	Leu	Leu	Lys	Ala	Ser	Gln
				95					100				105	
Gly	Phe	Ser	Leu	Phe	Leu	Gly	Ser	Lys	Tyr	Leu	Glu	Leu	Gln	Glu
				110					115				120	
Pro	Ser	Trp	Ser	Gly	Pro	Cys	Pro	Pro	Gly	Gln	Leu	His	Cys	Thr
				125					130				135	
Cys	Gly	Val	Leu	Leu	Ser	Phe	Leu							

<210> 303
<211> 1768
<212> DNA
<213> Homo sapiens

<400> 303
ggctggactg gaactcctgg tcccaagtga tccacccgcc tcagcctccc 50
aaggtgctgt gattataggt gtaagccacc gtgtctggcc tctgaacaac 100
ttttcagca actaaaaaaag ccacaggagt tgaactgcta ggattctgac 150
tatgctgtgg tggctagtgc tcctactcct acctacatta aaatctgttt 200
tttggttctct tgtaacttagc ctttacccctc ctaacacaga ggatctgtca 250
ctgtggctct ggcccaaacc tgacccac tctggaacga gaacagaggt 300
ttctacccac accgtccccct cgaagccggg gacagcctca ccttgctggc 350
ctctcgctgg agcagtgcac tcaccaactg tctcacgtct ggaggcactg 400
actcgggcag tgcaggttagc tgagcctctt gtagctgcg gctttcaagg 450
tgggccttgc cctggccgta gaagggattt acaagccga agatttcata 500
ggcgatggct cccactgccc aggcatcagc cttgctgttag tcaatcactg 550
ccctggggcc aggacgggccc gtggacacct gctcagaagc agtgggttag 600
acatcacgct gcccggccat ctaacccttt catgtcctgc acatcacctg 650
atccatgggc taatctgaac tctgtccaa ggaacccaga gcttgagtga 700
gctgtggctc agacccagaa ggggtctgct tagaccacct ggtttatgtg 750
acaggacttg catttcctg gaacatgagg gaacgcccga ggaaagcaaa 800
gtggcagggaa aggaacttgt gccaaattat gggcagaaaa agatggaggt 850
gttgggttat cacaaggcat cgagtctcct gcattcagtg gacatgtggg 900
ggaagggctg ccgatggcgc atgacacact cgggactcac ctctggggcc 950
atcagacagc cggttccgccc ccgatccacg taccagctgc tgaagggcaa 1000
ctgcaggccg atgctctcat cagccaggca gcagccaaaa tctgcgatca 1050
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ctccccctcct tccctctgag agggccctcct atgtccctac taaagccacc 1150
agcaagacat agctgacagg ggctaattggc tcagtgttgg cccaggaggt 1200
cagcaaggcc tgagagctga tcagaaggcc ctgctgtgcg aacacggaaa 1250

tgccctccagt aagcacaggc tgcaaaatcc ccaggcaaag gactgtgtgg 1300
ctcaatttaa atcatgttct agtaattgga gctgtcccca agaccaaagg 1350
agcttagagct tggttcaaata gatctccaag ggcccttata ccccaggaga 1400
ctttgatttg aatttgaaac cccaaatcca aacctaagaa ccaggtgcat 1450
taagaatcag ttattgccgg gtgtggtggc ctgtaatgcc aacatttgg 1500
gaggccgagg cgggttagatc acctgaggc aggagttcaa gaccagcctg 1550
gccaacatgg tgaaaccct gtctctacta aaaatacataaaaactagcc 1600
aggcatggtg gtgtgtgcct gtatcccagc tactcgggag gctgagacag 1650
gagaattact tgaacctggg aggtgaagga ggctgagaca ggagaatcac 1700
ttcagcctga gcaacacacgc gagactctgt ctcagaaaaa ataaaaaaag 1750
aattatggtt atttgtaa 1768

<210> 304

<211> 109

<212> PRT

<213> Homo sapiens

<400> 304

Met	Leu	Trp	Trp	Leu	Val	Leu	Leu	Leu	Leu	Pro	Thr	Leu	Lys	Ser
1					5				10				15	
Val	Phe	Cys	Ser	Leu	Val	Thr	Ser	Leu	Tyr	Leu	Pro	Asn	Thr	Glu
					20				25				30	
Asp	Leu	Ser	Leu	Trp	Leu	Trp	Pro	Lys	Pro	Asp	Leu	His	Ser	Gly
					35				40				45	
Thr	Arg	Thr	Glu	Val	Ser	Thr	His	Thr	Val	Pro	Ser	Lys	Pro	Gly
					50				55				60	
Thr	Ala	Ser	Pro	Cys	Trp	Pro	Leu	Ala	Gly	Ala	Val	Pro	Ser	Pro
					65				70				75	
Thr	Val	Ser	Arg	Leu	Glu	Ala	Leu	Thr	Arg	Ala	Val	Gln	Val	Ala
					80				85				90	
Glu	Pro	Leu	Gly	Ser	Cys	Gly	Phe	Gln	Gly	Gly	Pro	Cys	Pro	Gly
					95				100				105	
Arg	Arg	Arg	Asp											

<210> 305

<211> 989

<212> DNA

<213> Homo sapiens

<400> 305

gcggggccgc gagtccgaga cctgtcccag gagctccagc tcacgtgacc 50
tgtcaactgcc tccccccgccc tcctgcccgc gccatgacccc agccggtgcc 100
ccggctctcc gtgcccgcg cgctggccct gggctcagcc gcactggcg 150
ccgccttcgc cactggcctc ttccctggga ggcggtgccc cccatggcga 200
ggccggcgag agcagtgcct gttttttttt gaggacagcc gcctgtggca 250
gtatcttctg agccgctcca tgccggagca cccggcgctg cgaaggctga 300
ggctgctgac cctggagcag ccgcaggggg attctatgtat gacctgcgag 350
caggcccagc tcttggccaa cctggcgccg ctcatccagg ccaagaaggc 400
gctggacactg ggcaccttca cgggctactc cgcgcctggcc ctggccctgg 450
cgctgcccgc ggacgggcgc gtgggtaccc gcgaggtgga cgccgcagccc 500
ccggagctgg gacggccctt gtggaggcag gccgaggcgg agcacaagat 550
cgacctccgg ctgaagcccg ccttggagac cctggacgag ctgctggcg 600
cggcgaggc cggcaccttc gacgtggccg tgggtggatgc ggacaaggag 650
aactgctccg cctactacga gcgctgcctg cagctgctgc gacccggagg 700
catcctcgcc gtcctcagag tcctgtggcg cgggaagggtg ctgcaacctc 750
cgaaaggggc cgtggcgcc gagtgtgtgc gaaacctaaa cgaacgcac 800
cggcgggacg tcagggctta catcagcctc ctgcccctgg gcgtatggact 850
caccttggcc ttcaagatct agggctggcc cctagtgagt gggctcgagg 900
gagggttgcc tggaaacccc aggaattgac cctgagttt aaattcgaaa 950
ataaaagtggg gctgggacac aaaaaaaaaa aaaaaaaaaa 989

<210> 306

<211> 262

<212> PRT

<213> Homo sapiens

<400> 306

Met	Thr	Gln	Pro	Val	Pro	Arg	Leu	Ser	Val	Pro	Ala	Ala	Leu	Ala
1									10					15
Leu	Gly	Ser	Ala	Ala	Leu	Gly	Ala	Ala	Phe	Ala	Thr	Gly	Leu	Phe
									25					30
Leu	Gly	Arg	Arg	Cys	Pro	Pro	Trp	Arg	Gly	Arg	Arg	Glu	Gln	Cys
				35					40					45
Leu	Leu	Pro	Pro	Glu	Asp	Ser	Arg	Leu	Trp	Gln	Tyr	Leu	Leu	Ser
									55					60

Arg Ser Met Arg Glu His Pro Ala Leu Arg Ser Leu Arg Leu Leu
 65 70 75
 Thr Leu Glu Gln Pro Gln Gly Asp Ser Met Met Thr Cys Glu Gln
 80 85 90
 Ala Gln Leu Leu Ala Asn Leu Ala Arg Leu Ile Gln Ala Lys Lys
 95 100 105
 Ala Leu Asp Leu Gly Thr Phe Thr Gly Tyr Ser Ala Leu Ala Leu
 110 115 120
 Ala Leu Ala Leu Pro Ala Asp Gly Arg Val Val Thr Cys Glu Val
 125 130 135
 Asp Ala Gln Pro Pro Glu Leu Gly Arg Pro Leu Trp Arg Gln Ala
 140 145 150
 Glu Ala Glu His Lys Ile Asp Leu Arg Leu Lys Pro Ala Leu Glu
 155 160 165
 Thr Leu Asp Glu Leu Leu Ala Ala Gly Glu Ala Gly Thr Phe Asp
 170 175 180
 Val Ala Val Val Asp Ala Asp Lys Glu Asn Cys Ser Ala Tyr Tyr
 185 190 195
 Glu Arg Cys Leu Gln Leu Leu Arg Pro Gly Gly Ile Leu Ala Val
 200 205 210
 Leu Arg Val Leu Trp Arg Gly Lys Val Leu Gln Pro Pro Lys Gly
 215 220 225
 Asp Val Ala Ala Glu Cys Val Arg Asn Leu Asn Glu Arg Ile Arg
 230 235 240
 Arg Asp Val Arg Val Tyr Ile Ser Leu Leu Pro Leu Gly Asp Gly
 245 250 255
 Leu Thr Leu Ala Phe Lys Ile
 260

<210> 307
 <211> 2272
 <212> DNA
 <213> Homo sapiens

<400> 307
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 ctctcgccgt cagcatgcca cacgccttca agccccggga cttgggtttc 100
 gctaagatga agggctaccc tcactggcct gccaggatcg acgacatcgc 150
 ggatggcgcc gtgaagcccc cacccaaacaa gtaccccatc tttttctttg 200
 gcacacacga aacagccttc ctgggaccca aggacctgtt cccctacgac 250

aaatgtaaag acaagtacgg gaagcccaac aagaggaaag gttcaatga 300
agggctgtgg gagatccaga acaacccca cgccagctac agcgccctc 350
cgccagttag ctcctccgac agcgaggccc ccgaggccaa ccccgccgac 400
ggcagtgacg ctgacgagga cgtgaggac cggggggta tggccgtcac 450
agcgtaacc gccacagctg ccagcgacag gatggagagc gactcagact 500
cagacaagag tagcgacaac agtggcctga agaggaagac gcctgcgcta 550
aagatgtcg tctgaaacg agcccgaaag gcctccagcg acctggatca 600
ggccagcgtg tccccatccg aagaggagaa ctcggaaagc tcattctgagt 650
cgagaagac cagcgaccag gacttcacac ctgagaagaa agcagcggc 700
cggcgccac ggaggggccc tctgggggaa cggaaaaaaa agaaggcgcc 750
gtcagcctcc gactccgact ccaaggccga ttccggacggg gccaagcctg 800
agccggtgtgc catggcgcgg tcggcgtcct ctcctccctc ttccctcc 850
tcctccgact ccgtatgttc tgtgaagaag ctcggaggg gcaggaagcc 900
agcgagaag cctctcccgaa agcccgagg gcggaaacccg aacgcctgaac 950
ggcctccgtc cagctccagc agtgcacgtg acagcgacga ggtggaccgc 1000
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cagttagatc aagtttgcct taaaggtcga cagccggac gtgaagaggt 1550
gcctgaatgc cctagaggag ctggaaaccc tgcaggtgac ctctcagatc 1600
ctccagaaga acacagacgt ggtggccacc ttgaagaaga ttccgggtta 1650
caaagcgaac aaggacgtaa tggagaaggc agcagaagtc tataccggc 1700

tcaagtcgcg ggtcctcgcc ccaaagatcg aggccgtgca gaaagtgaac 1750
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gcagagcaga gaactgtggg gaacgctgtg ctgttgtat ttgttccctt 2200
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actataaacg gtttttaat ga 2272

<210> 308

<211> 671

<212> PRT

<213> Homo sapiens

<400> 308

Met	Pro	His	Ala	Phe	Lys	Pro	Gly	Asp	Leu	Val	Phe	Ala	Lys	Met
1					5				10				15	
Lys	Gly	Tyr	Pro	His	Trp	Pro	Ala	Arg	Ile	Asp	Asp	Ile	Ala	Asp
					20				25				30	
Gly	Ala	Val	Lys	Pro	Pro	Pro	Asn	Lys	Tyr	Pro	Ile	Phe	Phe	Phe
			35					40					45	
Gly	Thr	His	Glu	Thr	Ala	Phe	Leu	Gly	Pro	Lys	Asp	Leu	Phe	Pro
			50					55					60	
Tyr	Asp	Lys	Cys	Lys	Asp	Lys	Tyr	Gly	Lys	Pro	Asn	Lys	Arg	Lys
			65					70					75	
Gly	Phe	Asn	Glu	Gly	Leu	Trp	Glu	Ile	Gln	Asn	Asn	Pro	His	Ala
			80					85					90	
Ser	Tyr	Ser	Ala	Pro	Pro	Pro	Val	Ser	Ser	Ser	Asp	Ser	Glu	Ala
			95					100					105	
Pro	Glu	Ala	Asn	Pro	Ala	Asp	Gly	Ser	Asp	Ala	Asp	Glu	Asp	Asp
			110					115					120	
Glu	Asp	Arg	Gly	Val	Met	Ala	Val	Thr	Ala	Val	Thr	Ala	Thr	Ala
			125					130					135	
Ala	Ser	Asp	Arg	Met	Glu	Ser	Asp	Ser	Asp	Ser	Asp	Lys	Ser	Ser

140	145	150
Asp Asn Ser Gly Leu Lys Arg Lys Thr	Pro Ala Leu Lys Met	Ser
155	160	165
Val Ser Lys Arg Ala Arg Lys Ala Ser	Ser Asp Leu Asp Gln	Ala
170	175	180
Ser Val Ser Pro Ser Glu Glu Asn	Ser Glu Ser Ser Ser	Glu
185	190	195
Ser Glu Lys Thr Ser Asp Gln Asp Phe	Thr Pro Glu Lys Lys Ala	
200	205	210
Ala Val Arg Ala Pro Arg Arg Gly Pro	Leu Gly Gly Arg Lys Lys	
215	220	225
Lys Lys Ala Pro Ser Ala Ser Asp Ser	Asp Ser Lys Ala Asp Ser	
230	235	240
Asp Gly Ala Lys Pro Glu Pro Val Ala	Met Ala Arg Ser Ala Ser	
245	250	255
Ser Ser Ser Ser Ser Ser Ser Asp Ser Asp Val Ser Val		
260	265	270
Lys Lys Pro Pro Arg Gly Arg Lys Pro	Ala Glu Lys Pro Leu Pro	
275	280	285
Lys Pro Arg Gly Arg Lys Pro Lys Pro	Glu Arg Pro Pro Ser Ser	
290	295	300
Ser Ser Ser Asp Ser Asp Ser Asp Glu	Val Asp Arg Ile Ser Glu	
305	310	315
Trp Lys Arg Arg Asp Glu Ala Arg Arg	Arg Glu Leu Glu Ala Arg	
320	325	330
Arg Arg Arg Glu Gln Glu Glu Leu	Arg Arg Leu Arg Glu Gln	
335	340	345
Glu Lys Glu Glu Lys Glu Arg Arg	Glu Arg Ala Asp Arg Gly	
350	355	360
Glu Ala Glu Arg Gly Ser Gly Ser	Gly Asp Glu Leu Arg	
365	370	375
Glu Asp Asp Glu Pro Val Lys Lys Arg	Gly Arg Lys Gly Arg Gly	
380	385	390
Arg Gly Pro Pro Ser Ser Ser Asp Ser	Glu Pro Glu Ala Glu Leu	
395	400	405
Glu Arg Glu Ala Lys Lys Ser Ala Lys	Lys Pro Gln Ser Ser Ser	
410	415	420
Thr Glu Pro Ala Arg Lys Pro Gly Gln	Lys Glu Lys Arg Val Arg	
425	430	435

Pro Glu Glu Lys Gln Gln Ala Lys Pro Val Lys Val Glu Arg Thr
 440 445 450
 Arg Lys Arg Ser Glu Gly Phe Ser Met Asp Arg Lys Val Glu Lys
 455 460 465
 Lys Lys Glu Pro Ser Val Glu Glu Lys Leu Gln Lys Leu His Ser
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 Glu Ile Lys Phe Ala Leu Lys Val Asp Ser Pro Asp Val Lys Arg
 485 490 495
 Cys Leu Asn Ala Leu Glu Glu Leu Gly Thr Leu Gln Val Thr Ser
 500 505 510
 Gln Ile Leu Gln Lys Asn Thr Asp Val Val Ala Thr Leu Lys Lys
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 Ile Arg Arg Tyr Lys Ala Asn Lys Asp Val Met Glu Lys Ala Ala
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 Glu Val Tyr Thr Arg Leu Lys Ser Arg Val Leu Gly Pro Lys Ile
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 Glu Ala Val Gln Lys Val Asn Lys Ala Gly Met Glu Lys Glu Lys
 560 565 570
 Ala Glu Glu Lys Leu Ala Gly Glu Glu Leu Ala Gly Glu Glu Ala
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 Pro Gln Glu Lys Ala Glu Asp Lys Pro Ser Thr Asp Leu Ser Ala
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 Pro Val Asn Gly Glu Ala Thr Ser Gln Lys Gly Glu Ser Ala Glu
 605 610 615
 Asp Lys Glu His Glu Glu Gly Arg Asp Ser Glu Glu Gly Pro Arg
 620 625 630
 Cys Gly Ser Ser Glu Asp Leu His Asp Ser Val Arg Glu Gly Pro
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<210> 309
 <211> 3871
 <212> DNA
 <213> Homo sapiens

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<210> 310

<211> 777

<212> PRT

<213> Homo sapiens

<400> 310

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Phe	Leu	Pro	Val	Thr	Gly	Thr	Leu	Lys	Gln	Asn	Ile	Pro	Arg	Leu
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Lys	Leu	Thr	Tyr	Lys	Asp	Leu	Leu	Ser	Asn	Ser	Cys	Ile	Pro	
								50						60

Phe	Leu	Gly	Ser	Ser	Glu	Gly	Leu	Asp	Phe	Gln	Thr	Leu	Leu	Leu
								65						75

Asp Glu Glu Arg Gly Arg Leu Leu Leu Gly Ala Lys Asp His Ile

80	85	90
Phe Leu Leu Ser Leu Val Asp Leu Asn Lys	Asn Phe Lys Lys	Ile
95	100	105
Tyr Trp Pro Ala Ala Lys Glu Arg Val Glu	Leu Cys Lys Leu Ala	
110	115	120
Gly Lys Asp Ala Asn Thr Glu Cys Ala Asn	Phe Ile Arg Val Leu	
125	130	135
Gln Pro Tyr Asn Lys Thr His Ile Tyr Val	Cys Gly Thr Gly Ala	
140	145	150
Phe His Pro Ile Cys Gly Tyr Ile Asp Leu	Gly Val Tyr Lys Glu	
155	160	165
Asp Ile Ile Phe Lys Leu Asp Thr His Asn	Leu Glu Ser Gly Arg	
170	175	180
Leu Lys Cys Pro Phe Asp Pro Gln Gln	Pro Phe Ala Ser Val Met	
185	190	195
Thr Asp Glu Tyr Leu Tyr Ser Gly Thr Ala	Ser Asp Phe Leu Gly	
200	205	210
Lys Asp Thr Ala Phe Thr Arg Ser Leu	Gly Pro Thr His Asp His	
215	220	225
His Tyr Ile Arg Thr Asp Ile Ser Glu	His Tyr Trp Leu Asn Gly	
230	235	240
Ala Lys Phe Ile Gly Thr Phe Phe Ile	Pro Asp Thr Tyr Asn Pro	
245	250	255
Asp Asp Asp Lys Ile Tyr Phe Phe Arg	Glu Ser Ser Gln Glu	
260	265	270
Gly Ser Thr Ser Asp Lys Thr Ile Leu	Ser Arg Val Gly Arg Val	
275	280	285
Cys Lys Asn Asp Val Gly Gly Gln Arg	Ser Leu Ile Asn Lys Trp	
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Thr Thr Phe Leu Lys Ala Arg Leu Ile	Cys Ser Ile Pro Gly Ser	
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Asp Gly Ala Asp Thr Tyr Phe Asp Glu	Leu Gln Asp Ile Tyr Leu	
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Leu Pro Thr Arg Asp Glu Arg Asn Pro	Val Val Tyr Gly Val Phe	
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365	370	375

Lys Glu Ser Ala Asp His Arg Trp Val Gln Tyr Asp Gly Arg Ile
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 395 400 405
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 410 415 420
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 425 430 435
 Gly Gly Pro Thr Phe Lys Arg Ile Asn Val Asp Tyr Arg Leu Thr
 440 445 450
 Gln Ile Val Val Asp His Val Ile Ala Glu Asp Gly Gln Tyr Asp
 455 460 465
 Val Met Phe Leu Gly Thr Asp Ile Gly Thr Val Leu Lys Val Val
 470 475 480
 Ser Ile Ser Lys Glu Lys Trp Asn Met Glu Glu Val Val Leu Glu
 485 490 495
 Glu Leu Gln Ile Phe Lys His Ser Ser Ile Ile Leu Asn Met Glu
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 Cys Ala Asp Cys Cys Leu Ala Arg Asp Pro Tyr Cys Ala Trp Asp
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 Gly Asn Ala Cys Ser Arg Tyr Ala Pro Thr Ser Lys Arg Arg Ala
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 Arg Arg Gln Asp Val Lys Tyr Gly Asp Pro Ile Thr Gln Cys Trp
 575 580 585
 Asp Ile Glu Asp Ser Ile Ser His Glu Thr Ala Asp Glu Lys Val
 590 595 600
 Ile Phe Gly Ile Glu Phe Asn Ser Thr Phe Leu Glu Cys Ile Pro
 605 610 615
 Lys Ser Gln Gln Ala Thr Ile Lys Trp Tyr Ile Gln Arg Ser Gly
 620 625 630
 Asp Glu His Arg Glu Glu Leu Lys Pro Asp Glu Arg Ile Ile Lys
 635 640 645
 Thr Glu Tyr Gly Leu Leu Ile Arg Ser Leu Gln Lys Lys Asp Ser
 650 655 660
 Gly Met Tyr Tyr Cys Lys Ala Gln Glu His Thr Phe Ile His Thr

665	670	675
Ile Val Lys Leu Thr Leu Asn Val Ile Glu Asn Glu Gln Met Glu		
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Asn Thr Gln Arg Ala Glu His Glu Glu Gly Gln Val Lys Asp Leu		
695	700	705
Leu Ala Glu Ser Arg Leu Arg Tyr Lys Asp Tyr Ile Gln Ile Leu		
710	715	720
Ser Ser Pro Asn Phe Ser Leu Asp Gln Tyr Cys Glu Gln Met Trp		
725	730	735
His Arg Glu Lys Arg Arg Gln Arg Asn Lys Gly Gly Pro Lys Trp		
740	745	750
Lys His Met Gln Glu Met Lys Lys Arg Asn Arg Arg His His		
755	760	765
Arg Asp Leu Asp Glu Leu Pro Arg Ala Val Ala Thr		
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<210> 311

<211> 25

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-25

<223> Synthetic construct.

<400> 311

caacgcagcc gtgataaaca agtgg 25

<210> 312

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 312

gcttggacat gtaccaggcc gtgg 24

<210> 313

<211> 45

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-45

<223> Synthetic construct.

<400> 313
ggccagactg atttgctcaa ttccctggaag tcatggggca gatac 45

<210> 314
<211> 3934
<212> DNA
<213> Homo sapiens

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<210> 315

<211> 370

<212> PRT

<213> Homo sapiens

<400> 315

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Pro Ser Ile Glu Gln Arg Leu Gln Glu Val Arg Glu Ser Ile Arg
 50 55 60

Arg Ala Gln Val Ser Gln Val Lys Gly Ala Ala Arg Leu Ala Leu
 65 70 75

Leu Gln Gly Ala Gly Leu Asp Val Glu Arg Trp Leu Lys Pro Ala
 80 85 90

Met Thr Gln Ala Gln Asp Glu Val Glu Gln Glu Arg Arg Leu Ser
 95 100 105

Glu Ala Arg Leu Ser Gln Arg Asp Leu Ser Pro Thr Ala Glu Asp
 110 115 120

Ala Glu Leu Ser Asp Phe Glu Glu Cys Glu Glu Thr Gly Glu Leu
 125 130 135

Phe Glu Glu Pro Ala Pro Gln Ala Leu Ala Thr Arg Ala Leu Pro
 140 145 150

Cys Pro Ala His Val Val Phe Arg Tyr Gln Ala Gly Arg Glu Asp
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Glu Leu Thr Ile Thr Glu Gly Glu Trp Leu Glu Val Ile Glu Glu
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Gly Asp Ala Asp Glu Trp Val Lys Ala Arg Asn Gln His Gly Glu
 185 190 195

Val Gly Phe Val Pro Glu Arg Tyr Leu Asn Phe Pro Asp Leu Ser
 200 205 210

Leu Pro Glu Ser Ser Gln Asp Ser Asp Asn Pro Cys Gly Ala Glu
 215 220 225

Pro Thr Ala Phe Leu Ala Gln Ala Leu Tyr Ser Tyr Thr Gly Gln
 230 235 240

Ser Ala Glu Glu Leu Ser Phe Pro Glu Gly Ala Leu Ile Arg Leu
 245 250 255

Leu Pro Arg Ala Gln Asp Gly Val Asp Asp Gly Phe Trp Arg Gly
 260 265 270

Glu Phe Gly Gly Arg Val Gly Val Phe Pro Ser Leu Leu Val Glu
 275 280 285

Glu Leu Leu Gly Pro Pro Gly Pro Pro Glu Leu Ser Asp Pro Glu
 290 295 300

Gln Met Leu Pro Ser Pro Ser Pro Ser Phe Ser Pro Pro Ala

305	310	315
Pro Thr Ser Val Leu Asp Gly Pro Pro Ala Pro Val Leu Pro Gly		
320	325	330
Asp Lys Ala Leu Asp Phe Pro Gly Phe Leu Asp Met Met Ala Pro		
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Arg Leu Arg Pro Met Arg Pro Pro Pro Pro Ala Lys Ala		
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Pro Asp Pro Gly His Pro Asp Pro Leu Thr		
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<210> 316

<211> 4407

<212> DNA

<213> Homo sapiens

<400> 316

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<210> 317

<211> 837

<212> PRT

<213> Homo sapiens

<400> 317

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Trp	Leu	Trp	Gly	Ala	Gln	Pro	Cys	Leu	Leu	Leu	Pro	Ile	Val	Pro
							20			25				30
Leu	Ser	Trp	Leu	Val	Trp	Leu	Leu	Leu	Leu	Leu	Ala	Ser	Leu	
							35			40				45
Leu	Pro	Ser	Ala	Arg	Leu	Ala	Ser	Pro	Leu	Pro	Arg	Glu	Glu	
					50				55				60	
Ile	Val	Phe	Pro	Glu	Lys	Leu	Asn	Gly	Ser	Val	Leu	Pro	Gly	Ser
					65				70					75
Gly	Ala	Pro	Ala	Arg	Leu	Leu	Cys	Arg	Leu	Gln	Ala	Phe	Gly	Glu
					80				85					90
Thr	Leu	Leu	Leu	Glu	Leu	Glu	Gln	Asp	Ser	Gly	Val	Gln	Val	Glu
					95				100					105
Gly	Leu	Thr	Val	Gln	Tyr	Leu	Gly	Gln	Ala	Pro	Glu	Leu	Leu	Gly
					110				115					120
Gly	Ala	Glu	Pro	Gly	Thr	Tyr	Leu	Thr	Gly	Thr	Ile	Asn	Gly	Asp
					125				130					135
Pro	Glu	Ser	Val	Ala	Ser	Leu	His	Trp	Asp	Gly	Gly	Ala	Leu	Leu

140	145	150
Gly Val Leu Gln Tyr Arg Gly Ala Glu	Leu His Leu Gln Pro Leu	
155	160	165
Glu Gly Gly Thr Pro Asn Ser Ala Gly	Gly Pro Gly Ala His Ile	
170	175	180
Leu Arg Arg Lys Ser Pro Ala Ser Gly	Gln Gly Pro Met Cys Asn	
185	190	195
Val Lys Ala Pro Leu Gly Ser Pro Ser	Pro Arg Pro Arg Arg Ala	
200	205	210
Lys Arg Phe Ala Ser Leu Ser Arg Phe	Val Glu Thr Leu Val Val	
215	220	225
Ala Asp Asp Lys Met Ala Ala Phe His	Gly Ala Gly Leu Lys Arg	
230	235	240
Tyr Leu Leu Thr Val Met Ala Ala Ala	Lys Ala Phe Lys His	
245	250	255
Pro Ser Ile Arg Asn Pro Val Ser Leu	Val Val Thr Arg Leu Val	
260	265	270
Ile Leu Gly Ser Gly Glu Glu Gly Pro	Gln Val Gly Pro Ser Ala	
275	280	285
Ala Gln Thr Leu Arg Ser Phe Cys Ala	Trp Gln Arg Gly Leu Asn	
290	295	300
Thr Pro Glu Asp Ser Gly Pro Asp His	Phe Asp Thr Ala Ile Leu	
305	310	315
Phe Thr Arg Gln Asp Leu Cys Gly Val	Ser Thr Cys Asp Thr Leu	
320	325	330
Gly Met Ala Asp Val Gly Thr Val Cys	Asp Pro Ala Arg Ser Cys	
335	340	345
Ala Ile Val Glu Asp Asp Gly Leu Gln	Ser Ala Phe Thr Ala Ala	
350	355	360
His Glu Leu Gly His Val Phe Asn Met	Leu His Asp Asn Ser Lys	
365	370	375
Pro Cys Ile Ser Leu Asn Gly Pro Leu	Ser Thr Ser Arg His Val	
380	385	390
Met Ala Pro Val Met Ala His Val Asp	Pro Glu Glu Pro Trp Ser	
395	400	405
Pro Cys Ser Ala Arg Phe Ile Thr Asp	Phe Leu Asp Asn Gly Tyr	
410	415	420
Gly His Cys Leu Leu Asp Lys Pro Glu	Ala Pro Leu His Leu Pro	
425	430	435

Val Thr Phe Pro Gly Lys Asp Tyr Asp Ala Asp Arg Gln Cys Gln
 440 445 450
 Leu Thr Phe Gly Pro Asp Ser Arg His Cys Pro Gln Leu Pro Pro
 455 460 465
 Pro Cys Ala Ala Leu Trp Cys Ser Gly His Leu Asn Gly His Ala
 470 475 480
 Met Cys Gln Thr Lys His Ser Pro Trp Ala Asp Gly Thr Pro Cys
 485 490 495
 Gly Pro Ala Gln Ala Cys Met Gly Gly Arg Cys Leu His Met Asp
 500 505 510
 Gln Leu Gln Asp Phe Asn Ile Pro Gln Ala Gly Gly Trp Gly Pro
 515 520 525
 Trp Gly Pro Trp Gly Asp Cys Ser Arg Thr Cys Gly Gly Gly Val
 530 535 540
 Gln Phe Ser Ser Arg Asp Cys Thr Arg Pro Val Pro Arg Asn Gly
 545 550 555
 Gly Lys Tyr Cys Glu Gly Arg Arg Thr Arg Phe Arg Ser Cys Asn
 560 565 570
 Thr Glu Asp Cys Pro Thr Gly Ser Ala Leu Thr Phe Arg Glu Glu
 575 580 585
 Gln Cys Ala Ala Tyr Asn His Arg Thr Asp Leu Phe Lys Ser Phe
 590 595 600
 Pro Gly Pro Met Asp Trp Val Pro Arg Tyr Thr Gly Val Ala Pro
 605 610 615
 Gln Asp Gln Cys Lys Leu Thr Cys Gln Ala Arg Ala Leu Gly Tyr
 620 625 630
 Tyr Tyr Val Leu Glu Pro Arg Val Val Asp Gly Thr Pro Cys Ser
 635 640 645
 Pro Asp Ser Ser Ser Val Cys Val Gln Gly Arg Cys Ile His Ala
 650 655 660
 Gly Cys Asp Arg Ile Ile Gly Ser Lys Lys Lys Phe Asp Lys Cys
 665 670 675
 Met Val Cys Gly Gly Asp Gly Ser Gly Cys Ser Lys Gln Ser Gly
 680 685 690
 Ser Phe Arg Lys Phe Arg Tyr Gly Tyr Asn Asn Val Val Thr Ile
 695 700 705
 Pro Ala Gly Ala Thr His Ile Leu Val Arg Gln Gln Gly Asn Pro
 710 715 720
 Gly His Arg Ser Ile Tyr Leu Ala Leu Lys Leu Pro Asp Gly Ser

725	730	735
Tyr Ala Leu Asn Gly Glu Tyr Thr Leu Met Pro Ser Pro Thr Asp		
740	745	750
Val Val Leu Pro Gly Ala Val Ser Leu Arg Tyr Ser Gly Ala Thr		
755	760	765
Ala Ala Ser Glu Thr Leu Ser Gly His Gly Pro Leu Ala Gln Pro		
770	775	780
Leu Thr Leu Gln Val Leu Val Ala Gly Asn Pro Gln Asp Thr Arg		
785	790	795
Leu Arg Tyr Ser Phe Phe Val Pro Arg Pro Thr Pro Ser Thr Pro		
800	805	810
Arg Pro Thr Pro Gln Asp Trp Leu His Arg Arg Ala Gln Ile Leu		
815	820	825
Glu Ile Leu Arg Arg Arg Pro Trp Ala Gly Arg Lys		
830	835	

<210> 318
<211> 23
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-23
<223> Synthetic construct.

<400> 318
ccctgaagct gccagatggc tcc 23

<210> 319
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 319
ctgtgcttt cggtgccagcc agtc 24

<210> 320
<211> 43
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-43
<223> Synthetic construct.

<400> 320
ccacagatgt ggtactgcct ggggcagtc a gttgcgcta cag 43

<210> 321
<211> 1197
<212> DNA
<213> Homo sapiens

<400> 321
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ctaaatgcag aagcttttaa atccaagaaa atatgtaaat cacttaagat 150
ttgtggactg gtgtttggta tcctggccct aactctaatt gtcctgttt 200
gggggagcaa gcacttctgg ccggaggtac ccaaaaaagc ctatgacatg 250
gagcacactt tctacagcaa tggagagaag aagaagattt acatggaaat 300
tgatcctgtg accagaactg aaatattcg aagcggaaat ggcactgatg 350
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gtgggtcttc aaaaatgttt tatcaaaact cagattaaag tgattcctga 450
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ctttcttga acagtcagtg atttgggtcc cagcagaaaa gcctattgaa 550
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atactgaaaa tggaaatagaa tttgatccca tgctggatga gagaggttat 850
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<210> 322

<211> 317
<212> PRT
<213> Homo sapiens

<400> 322

Met	Ala	Lys	Asn	Pro	Pro	Glu	Asn	Cys	Glu	Asp	Cys	His	Ile	Leu	
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Asn	Ala	Glu	Ala	Phe	Lys	Ser	Lys	Lys	Ile	Cys	Lys	Ser	Leu	Lys	
		20						25							30
Ile	Cys	Gly	Leu	Val	Phe	Gly	Ile	Leu	Ala	Leu	Thr	Leu	Ile	Val	
			35					40							45
Leu	Phe	Trp	Gly	Ser	Lys	His	Phe	Trp	Pro	Glu	Val	Pro	Lys	Lys	
			50					55							60
Ala	Tyr	Asp	Met	Glu	His	Thr	Phe	Tyr	Ser	Asn	Gly	Glu	Lys	Lys	
			65					70							75
Lys	Ile	Tyr	Met	Glu	Ile	Asp	Pro	Val	Thr	Arg	Thr	Glu	Ile	Phe	
			80					85							90
Arg	Ser	Gly	Asn	Gly	Thr	Asp	Glu	Thr	Leu	Glu	Val	His	Asp	Phe	
			95					100							105
Lys	Asn	Gly	Tyr	Thr	Gly	Ile	Tyr	Phe	Val	Gly	Leu	Gln	Lys	Cys	
			110					115							120
Phe	Ile	Lys	Thr	Gln	Ile	Lys	Val	Ile	Pro	Glu	Phe	Ser	Glu	Pro	
			125					130							135
Glu	Glu	Glu	Ile	Asp	Glu	Asn	Glu	Glu	Ile	Thr	Thr	Thr	Phe	Phe	
			140					145							150
Glu	Gln	Ser	Val	Ile	Trp	Val	Pro	Ala	Glu	Lys	Pro	Ile	Glu	Asn	
			155					160							165
Arg	Asp	Phe	Leu	Lys	Asn	Ser	Lys	Ile	Leu	Glu	Ile	Cys	Asp	Asn	
			170					175							180
Val	Thr	Met	Tyr	Trp	Ile	Asn	Pro	Thr	Leu	Ile	Ser	Val	Ser	Glu	
			185					190							195
Leu	Gln	Asp	Phe	Glu	Glu	Glu	Gly	Glu	Asp	Leu	His	Phe	Pro	Ala	
			200					205							210
Asn	Glu	Lys	Lys	Gly	Ile	Glu	Gln	Asn	Glu	Gln	Trp	Val	Val	Pro	
			215					220							225
Gln	Val	Lys	Val	Glu	Lys	Thr	Arg	His	Ala	Arg	Gln	Ala	Ser	Glu	
			230					235							240
Glu	Glu	Leu	Pro	Ile	Asn	Asp	Tyr	Thr	Glu	Asn	Gly	Ile	Glu	Phe	
			245					250							255
Asp	Pro	Met	Leu	Asp	Glu	Arg	Gly	Tyr	Cys	Cys	Ile	Tyr	Cys	Arg	
			260					265							270

Arg Gly Asn Arg Tyr Cys Arg Arg Val Cys Glu Pro Leu Leu Gly
275 280 285

Tyr Tyr Pro Tyr Pro Tyr Cys Tyr Gln Gly Gly Arg Val Ile Cys
290 295 300

Arg Val Ile Met Pro Cys Asn Trp Trp Val Ala Arg Met Leu Gly
305 310 315

Arg Val

<210> 323

<211> 1174

<212> DNA

<213> Homo sapiens

<400> 323

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<210> 324

<211> 239

<212> PRT

<213> Homo sapiens

<400> 324

Met	Ala	Ser	Thr	Ala	Val	Gln	Leu	Leu	Gly	Phe	Leu	Leu	Ser	Phe
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Leu	Gly	Met	Val	Gly	Thr	Leu	Ile	Thr	Thr	Ile	Leu	Pro	His	Trp
			20					25				30		
Arg	Arg	Thr	Ala	His	Val	Gly	Thr	Asn	Ile	Leu	Thr	Ala	Val	Ser
				35				40				45		
Tyr	Leu	Lys	Gly	Leu	Trp	Met	Glu	Cys	Val	Trp	His	Ser	Thr	Gly
				50				55			60			
Ile	Tyr	Gln	Cys	Gln	Ile	Tyr	Arg	Ser	Leu	Leu	Ala	Leu	Pro	Gln
				65				70			75			
Asp	Leu	Gln	Ala	Ala	Arg	Ala	Leu	Met	Val	Ile	Ser	Cys	Leu	Leu
				80				85			90			
Ser	Gly	Ile	Ala	Cys	Ala	Cys	Ala	Val	Ile	Gly	Met	Lys	Cys	Thr
				95				100			105			
Arg	Cys	Ala	Lys	Gly	Thr	Pro	Ala	Lys	Thr	Thr	Phe	Ala	Ile	Leu
				110				115			120			
Gly	Gly	Thr	Leu	Phe	Ile	Leu	Ala	Gly	Leu	Leu	Cys	Met	Val	Ala
				125				130			135			
Val	Ser	Trp	Thr	Thr	Asn	Asp	Val	Val	Gln	Asn	Phe	Tyr	Asn	Pro
				140				145			150			
Leu	Leu	Pro	Ser	Gly	Met	Lys	Phe	Glu	Ile	Gly	Gln	Ala	Leu	Tyr
				155				160			165			
Leu	Gly	Phe	Ile	Ser	Ser	Ser	Leu	Ser	Leu	Ile	Gly	Gly	Thr	Leu
				170				175			180			
Leu	Cys	Leu	Ser	Cys	Gln	Asp	Glu	Ala	Pro	Tyr	Arg	Pro	Tyr	Gln
				185				190			195			
Ala	Pro	Pro	Arg	Ala	Thr	Thr	Thr	Ala	Asn	Thr	Ala	Pro	Ala	
				200				205			210			
Tyr	Gln	Pro	Pro	Ala	Ala	Tyr	Lys	Asp	Asn	Arg	Ala	Pro	Ser	Val
				215				220			225			

Thr Ser Ala Thr His Ser Gly Tyr Arg Leu Asn Asp Tyr Val
230 235

<210> 325

<211> 2121

<212> DNA

<213> Homo sapiens

<400> 325

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<210> 326
<211> 261
<212> PRT
<213> Homo sapiens

<400> 326

Met Ser Thr Thr Cys Gln Val Val Ala Phe Leu Leu Ser Ile
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Leu Gly Leu Ala Gly Cys Ile Ala Ala Thr Gly Met Asp Met Trp
20 25 30

Ser Thr Gln Asp Leu Tyr Asp Asn Pro Val Thr Ser Val Phe Gln
35 40 45

Tyr Glu Gly Leu Trp Arg Ser Cys Val Arg Gln Ser Ser Gly Phe
50 55 60

Thr Glu Cys Arg Pro Tyr Phe Thr Ile Leu Gly Leu Pro Ala Met
65 70 75

Leu Gln Ala Val Arg Ala Leu Met Ile Val Gly Ile Val Leu Gly

80	85	90
Ala Ile Gly Leu Leu Val Ser Ile Phe Ala Leu Lys Cys Ile Arg		
95	100	105
Ile Gly Ser Met Glu Asp Ser Ala Lys Ala Asn Met Thr Leu Thr		
110	115	120
Ser Gly Ile Met Phe Ile Val Ser Gly Leu Cys Ala Ile Ala Gly		
125	130	135
Val Ser Val Phe Ala Asn Met Leu Val Thr Asn Phe Trp Met Ser		
140	145	150
Thr Ala Asn Met Tyr Thr Gly Met Gly Gly Met Val Gln Thr Val		
155	160	165
Gln Thr Arg Tyr Thr Phe Gly Ala Ala Leu Phe Val Gly Trp Val		
170	175	180
Ala Gly Gly Leu Thr Leu Ile Gly Gly Val Met Met Cys Ile Ala		
185	190	195
Cys Arg Gly Leu Ala Pro Glu Glu Thr Asn Tyr Lys Ala Val Ser		
200	205	210
Tyr His Ala Ser Gly His Ser Val Ala Tyr Lys Pro Gly Gly Phe		
215	220	225
Lys Ala Ser Thr Gly Phe Gly Ser Asn Thr Lys Asn Lys Lys Ile		
230	235	240
Tyr Asp Gly Gly Ala Arg Thr Glu Asp Glu Val Gln Ser Tyr Pro		
245	250	255
Ser Lys His Asp Tyr Val		
260		
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<212> DNA		
<213> Homo sapiens		
<400> 327		
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<210> 328
<211> 225
<212> PRT
<213> Homo sapiens

<400> 328

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					20				25					30
Arg	Val	Ser	Ala	Phe	Ile	Glu	Asn	Asn	Ile	Val	Val	Phe	Glu	Asn
					35				40					45
Phe	Trp	Glu	Gly	Leu	Trp	Met	Asn	Cys	Val	Arg	Gln	Ala	Asn	Ile
					50				55					60
Arg	Met	Gln	Cys	Lys	Ile	Tyr	Asp	Ser	Leu	Leu	Ala	Leu	Ser	Pro
					65				70					75
Asp	Leu	Gln	Ala	Ala	Arg	Gly	Leu	Met	Cys	Ala	Ala	Ser	Val	Met
					80				85					90
Ser	Phe	Leu	Ala	Phe	Met	Met	Ala	Ile	Leu	Gly	Met	Lys	Cys	Thr
					95				100					105
Arg	Cys	Thr	Gly	Asp	Asn	Glu	Lys	Val	Lys	Ala	His	Ile	Leu	Leu
					110				115					120
Thr	Ala	Gly	Ile	Ile	Phe	Ile	Ile	Thr	Gly	Met	Val	Val	Leu	Ile
					125				130					135
Pro	Val	Ser	Trp	Val	Ala	Asn	Ala	Ile	Ile	Arg	Asp	Phe	Tyr	Asn
					140				145					150
Ser	Ile	Val	Asn	Val	Ala	Gln	Lys	Arg	Glu	Leu	Gly	Glu	Ala	Leu
					155				160					165
Tyr	Leu	Gly	Trp	Thr	Thr	Ala	Leu	Val	Leu	Ile	Val	Gly	Gly	Ala
					170				175					180
Leu	Phe	Cys	Cys	Val	Phe	Cys	Cys	Asn	Glu	Lys	Ser	Ser	Ser	Tyr
					185				190					195
Arg	Tyr	Ser	Ile	Pro	Ser	His	Arg	Thr	Thr	Gln	Lys	Ser	Tyr	His
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Thr Gly Lys Lys Ser Pro Ser Val Tyr Ser Arg Ser Gln Tyr Val
215 220 225

<210> 329

<211> 1315

<212> DNA

<213> Homo sapiens

<400> 329

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gaccgctttc atcggcaaca gcatcgtggt ggcccaggtg gtgtgggagg 150
gcctgtggat gtcctgcgtg gtgcagagca ccggccagat gcagtgcaag 200
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gctaatacccc gtgtgctgga cggcgcatgc catcatccgg gacttctata 450
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ctgcacttgc ccctcggggg ggtcccaggg ccccagccat tacatggccc 600
gctactcaac atctgcccct gccatctc gggggccctc tgagtaccct 650
accaagaatt acgtctgacg tggagggaa tgggggctcc gctggcgcta 700
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tgttttgtta gtgca 1315

<210> 330

<211> 220

<212> PRT

<213> Homo sapiens

<400> 330

Met Ala Ser Ala Gly Met Gln Ile Leu Gly Val Val Leu Thr Leu
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Leu Gly Trp Val Asn Gly Leu Val Ser Cys Ala Leu Pro Met Trp
20 25 30

Lys Val Thr Ala Phe Ile Gly Asn Ser Ile Val Val Ala Gln Val
35 40 45

Val Trp Glu Gly Leu Trp Met Ser Cys Val Val Gln Ser Thr Gly
50 55 60

Gln Met Gln Cys Lys Val Tyr Asp Ser Leu Leu Ala Leu Pro Gln
65 70 75

Asp Leu Gln Ala Ala Arg Ala Leu Cys Val Ile Ala Leu Leu Val
80 85 90

Ala Leu Phe Gly Leu Leu Val Tyr Leu Ala Gly Ala Lys Cys Thr
95 100 105

Thr Cys Val Glu Glu Lys Asp Ser Lys Ala Arg Leu Val Leu Thr
110 115 120

Ser Gly Ile Val Phe Val Ile Ser Gly Val Leu Thr Leu Ile Pro
125 130 135

Val Cys Trp Thr Ala His Ala Ile Ile Arg Asp Phe Tyr Asn Pro
140 145 150

Leu Val Ala Glu Ala Gln Lys Arg Glu Leu Gly Ala Ser Leu Tyr
155 160 165

Leu Gly Trp Ala Ala Ser Gly Leu Leu Leu Gly Gly Gly Leu
170 175 180

Leu Cys Cys Thr Cys Pro Ser Gly Gly Ser Gln Gly Pro Ser His
185 190 195

Tyr Met Ala Arg Tyr Ser Thr Ser Ala Pro Ala Ile Ser Arg Gly
200 205 210

Pro Ser Glu Tyr Pro Thr Lys Asn Tyr Val
215 220

<210> 331

<211> 1160

<212> DNA

<213> Homo sapiens

<400> 331
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gttccttggc atgggggaa ctcttgc当地 aacccttctg cctcagtggt 200
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gcaagttcta tagtccttgc ttggctctcc cgcctgc当地 ggaaacagcc 350
cggccctca tgtgtgtggc tggctctcc tccttgatcg ccctgctt当地 400
tggcatctgt ggc当地 gaagc aggtccagtg cacaggctct aacgagaggg 450
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cactttccct tggctggca agcgctgctg tcctcttcat tggagggggt 650
ctgctttgtg gatttgtc当地 ctgcaacaga aagaagcaag ggtacagata 700
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ccaaagtatgg actatggta atgttttta taaagtgc当地 cttagaaactg 850
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cgaaagttc aatttggta tggggtagg aatgaaaatg acttacttgg 950
acattctgac ttcaaggta ttaaatgcat tgactatgt tggacc当地 1000
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caagtgtaca atgatggact acttattact tttgaccat catgtattat 1100
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acctattcta 1160

<210> 332

<211> 173

<212> PRT

<213> Homo sapiens

<400> 332

Met Asn Cys Ile Arg Gln Ala Arg Val Arg Leu Gln Cys Lys Phe

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Tyr Ser Ser Leu Leu Ala Leu Pro Pro Ala Leu Glu Thr Ala Arg			
20	25		30
Ala Leu Met Cys Val Ala Val Ala Leu Ser Leu Ile Ala Leu Leu			
35	40		45
Ile Gly Ile Cys Gly Met Lys Gln Val Gln Cys Thr Gly Ser Asn			
50	55		60
Glu Arg Ala Lys Ala Tyr Leu Leu Gly Thr Ser Gly Val Leu Phe			
65	70		75
Ile Leu Thr Gly Ile Phe Val Leu Ile Pro Val Ser Trp Thr Ala			
80	85		90
Asn Ile Ile Ile Arg Asp Phe Tyr Asn Pro Ala Ile His Ile Gly			
95	100		105
Gln Lys Arg Glu Leu Gly Ala Ala Leu Phe Leu Gly Trp Ala Ser			
110	115		120
Ala Ala Val Leu Phe Ile Gly Gly Leu Leu Cys Gly Phe Cys			
125	130		135
Cys Cys Asn Arg Lys Lys Gln Gly Tyr Arg Tyr Pro Val Pro Gly			
140	145		150
Tyr Arg Val Pro His Thr Asp Lys Arg Arg Asn Thr Thr Met Leu			
155	160		165
Ser Lys Thr Ser Thr Ser Tyr Val			
170			

<210> 333
 <211> 535
 <212> DNA
 <213> Homo sapiens

<400> 333
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 ctcagaagct gctagtctgt ctccaaaaaa agtggactgc agcatttaca 150
 agaagtatcc agtggtgcc atcccctgcc ccatcacata cctaccagtt 200
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 tcatcatccc aggctctgac tgagtttctt tcagtttac tgatgttctg 400
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ttctgtgcta cccctacaaa cccatgcctc actgacagac cagcatttt 500

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<210> 334

<211> 85

<212> PRT

<213> Homo sapiens

<400> 334

Met Lys Ile Thr Gly Gly Leu Leu Leu Cys Thr Val Val Tyr
1 5 10 15

Phe Cys Ser Ser Ser Glu Ala Ala Ser Leu Ser Pro Lys Lys Val
20 25 30

Asp Cys Ser Ile Tyr Lys Lys Tyr Pro Val Val Ala Ile Pro Cys
35 40 45

Pro Ile Thr Tyr Leu Pro Val Cys Gly Ser Asp Tyr Ile Thr Tyr
50 55 60

Gly Asn Glu Cys His Leu Cys Thr Glu Ser Leu Lys Ser Asn Gly
65 70 75

Arg Val Gln Phe Leu His Asp Gly Ser Cys
80 85

<210> 335

<211> 742

<212> DNA

<213> Homo sapiens

<400> 335

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ggcataagtg gaaataaaact caagctgatg cttcaaaaac gagaagcacc 200

tgttccaaact aagactaaag tggccgttga tgagaataaa gccaaagaat 250

tccttggcag cctgaagcgc cagaagccgc agctgtggga ccggactcgg 300

cccgagggtgc agcagtggta ccagcagttt ctctacatgg gctttgatga 350

agcgaaattt gaagatgaca tcacctattt gcttaacaga gatcgaaatg 400

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tttgcttat ttcagcagat cttttctacc tactttgtgt gatcaaaaaa 650
gaagagttaa aacaacacat gtaaatgcct tttgatattt catggaaatg 700
cctctcattt aaaaatagaa ataaagcatt ttgttaaaaa ga 742

<210> 336
<211> 148
<212> PRT
<213> Homo sapiens

<400> 336
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20 25 30
Gly Asn Lys Leu Lys Leu Met Leu Gln Lys Arg Glu Ala Pro Val
35 40 45
Pro Thr Lys Thr Lys Val Ala Val Asp Glu Asn Lys Ala Lys Glu
50 55 60
Phe Leu Gly Ser Leu Lys Arg Gln Lys Arg Gln Leu Trp Asp Arg
65 70 75
Thr Arg Pro Glu Val Gln Gln Trp Tyr Gln Gln Phe Leu Tyr Met
80 85 90
Gly Phe Asp Glu Ala Lys Phe Glu Asp Asp Ile Thr Tyr Trp Leu
95 100 105
Asn Arg Asp Arg Asn Gly His Glu Tyr Tyr Gly Asp Tyr Tyr Gln
110 115 120
Arg His Tyr Asp Glu Asp Ser Ala Ile Gly Pro Arg Ser Pro Tyr
125 130 135
Gly Phe Arg His Gly Ala Ser Val Asn Tyr Asp Asp Tyr
140 145

<210> 337
<211> 1310
<212> DNA
<213> Homo sapiens

<400> 337
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tgaagggtg ggtgatgagg tgaccgtcct tttctcggtg cttgcctgcc 150
ttctgggtct ggcccttgcc tgggtctcaa cgcacaccgc tgagggcggg 200
gacccactgc cccagccgtc agggacccca acgccccccc agcccagcgc 250

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cccccagcct gagacacaga ggtcaagctg cacagccaga gcccagcacg 350
gggttcacag caacaccgccc agccccggac tccccgcagg agcccctcgt 400
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cccacgacac cattggctcc ttgaaaagga cccagttcc cggccggaa 500
cagcaggtgc gactcatcta ccaagggcag ctgctaggcg acgacaccca 550
gaccctgggc agccttcacc tccctccaa ctgcgttctc cactgccacg 600
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gaggaccctggc ccgcctccaa tccctgacag ctccttggc tgagttgggg 1200
acgccaggtc ggtgggaggg tggtaaggg gagcggggag gggcagagga 1250
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<210> 338

<211> 246

<212> PRT

<213> Homo sapiens

<400> 338

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				20					25					30
Thr	His	Thr	Ala	Glu	Gly	Gly	Asp	Pro	Leu	Pro	Gln	Pro	Ser	Gly
				35				40						45

Thr	Pro	Thr	Pro	Ser	Gln	Pro	Ser	Ala	Ala	Met	Ala	Ala	Thr	Asp
								50		55			60	
Ser	Met	Arg	Gly	Glu	Ala	Pro	Gly	Ala	Glu	Thr	Pro	Ser	Leu	Arg
								65		70			75	
His	Arg	Gly	Gln	Ala	Ala	Gln	Pro	Glu	Pro	Ser	Thr	Gly	Phe	Thr
								80		85			90	
Ala	Thr	Pro	Pro	Ala	Pro	Asp	Ser	Pro	Gln	Glu	Pro	Leu	Val	Leu
								95		100			105	
Arg	Leu	Lys	Phe	Leu	Asn	Asp	Ser	Glu	Gln	Val	Ala	Arg	Ala	Trp
								110		115			120	
Pro	His	Asp	Thr	Ile	Gly	Ser	Leu	Lys	Arg	Thr	Gln	Phe	Pro	Gly
								125		130			135	
Arg	Glu	Gln	Gln	Val	Arg	Leu	Ile	Tyr	Gln	Gly	Gln	Leu	Leu	Gly
								140		145			150	
Asp	Asp	Thr	Gln	Thr	Leu	Gly	Ser	Leu	His	Leu	Pro	Pro	Asn	Cys
								155		160			165	
Val	Leu	His	Cys	His	Val	Ser	Thr	Arg	Val	Gly	Pro	Pro	Asn	Pro
								170		175			180	
Pro	Cys	Pro	Pro	Gly	Ser	Glu	Pro	Gly	Pro	Ser	Gly	Leu	Glu	Ile
								185		190			195	
Gly	Ser	Leu	Leu	Leu	Pro	Leu								
								200		205			210	
Trp	Tyr	Cys	Gln	Ile	Gln	Tyr	Arg	Pro	Phe	Phe	Pro	Leu	Thr	Ala
								215		220			225	
Thr	Leu	Gly	Leu	Ala	Gly	Phe	Thr	Leu	Leu	Leu	Ser	Leu	Leu	Ala
								230		235			240	
Phe	Ala	Met	Tyr	Arg	Pro									
								245						

<210> 339

<211> 849

<212> DNA

<213> Homo sapiens

<400> 339

gagattggaa acagccaggt tggagcagtg agtgagtaag gaaacctggc 50

tgcctctcc agattccccca ggctctcaga gaagatcagc agaaaagtctg 100

caagacccta agaaccatca gcccctcagct gcacccctc cccctccaagg 150

atgacaaagg cgctactcat ctatggtc agcagcttc ttgcctaaa 200

tcaggccagc ctcatcagtc gctgtgactt ggcccaggtg ctgcagctgg 250

aggacttgg a tgggtttgag ggttactccc t gaggactg gctgtgcctg 300
gctttgtgg a aagcaagtt caacatatca a agataaatg aaaatgcgga 350
t ggaagctt gactatggcc t cttccagat caacagccac tactggtgca 400
acgattataa gagttactcg gaaaacctt gccacgtaga ctgtcaagat 450
ctgctgaatc ccaaccttct tgcaggcatc cactgcgcaa aaaggattgt 500
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ccttcccatt tacaactaaa actgaccaga gccccagaa taaatggttt 750
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t gttatttgtt aaactgagga ccacaataaa gaaatcttta tatttatcg 849

<210> 340

<211> 148

<212> PRT

<213> Homo sapiens

<400> 340

Met	Thr	Lys	Ala	Leu	Leu	Ile	Tyr	Leu	Val	Ser	Ser	Phe	Leu	Ala
1				5					10					15
Leu	Asn	Gln	Ala	Ser	Leu	Ile	Ser	Arg	Cys	Asp	Leu	Ala	Gln	Val
				20					25					30
Leu	Gln	Leu	Glu	Asp	Leu	Asp	Gly	Phe	Glu	Gly	Tyr	Ser	Leu	Ser
				35					40					45
Asp	Trp	Leu	Cys	Leu	Ala	Phe	Val	Glu	Ser	Lys	Phe	Asn	Ile	Ser
				50				55						60
Lys	Ile	Asn	Glu	Asn	Ala	Asp	Gly	Ser	Phe	Asp	Tyr	Gly	Leu	Phe
				65				70						75
Gln	Ile	Asn	Ser	His	Tyr	Trp	Cys	Asn	Asp	Tyr	Lys	Ser	Tyr	Ser
				80				85						90
Glu	Asn	Leu	Cys	His	Val	Asp	Cys	Gln	Asp	Leu	Leu	Asn	Pro	Asn
				95				100						105
Leu	Leu	Ala	Gly	Ile	His	Cys	Ala	Lys	Arg	Ile	Val	Ser	Gly	Ala
				110					115					120
Arg	Gly	Met	Asn	Asn	Trp	Val	Glu	Trp	Arg	Leu	His	Cys	Ser	Gly
				125				130						135
Arg	Pro	Leu	Ser	Tyr	Trp	Leu	Thr	Gly	Cys	Arg	Leu	Arg		

<210> 341
<211> 23
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-23
<223> Synthetic construct.

<400> 341
ccctccaagg atgacaaaagg cgc 23

<210> 342
<211> 29
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-29
<223> Synthetic construct.

<400> 342
ggtcagcagc tttcttgccc taaatcagg 29

<210> 343
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 343
atctcaggcg gcatcctgtc agcc 24

<210> 344
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 344
gtggatgcct gcaagaaggt tggg 24

<210> 345
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 345
actttctg ccctaaatca ggccagcctc atcagtcgct gtgac 45

<210> 346
<211> 2575
<212> DNA
<213> Homo sapiens

<400> 346
tctgaccta ctggaagcgt ccaaagaggg acggctgtca gcccgttg 50
actgagaacc caccagctca tcccagacac ctcatagcaa cctattata 100
caaaggggaa aagaaacacc tgagcagaat ggaatcatta ttttttccc 150
aaggagaaaa ccgggttaaa gggagggaaag caattcaatt tgaagtccct 200
gtgaatgggc tttcagaagg caattaaaga aatccactca gagaggactt 250
ggggtaaac ttgggtcctg tggtttctg attgttaagtg gaagcaggtc 300
ttgcacacgc tggtggcaaa tgtcaggacc aggttaagtg actggcagaa 350
aaactccag gtggaacaag caacccatgt tctgctgcaa gcttgaagga 400
gcctggagcg ggagaaagct aacttgaaca tgacctgttgcatttggca 450
gttctagcaa catgctccta aggaagcgat acaggcacag accatgcaga 500
ctccagttcc tcctgctgct cctgatgctg ggatgcgtcc tcatgtatgg 550
ggcgatgttgc caccctcccc accacaccct gcaccagact gtcacagccc 600
aagccagcaa gcacagccct gaagccaggt accgcctgga ctttgggaa 650
tcccaggatt gggtaactgga agctgaggat gagggtaag agtacagccc 700
tctggagggc ctgccaccct ttatctact gcggggaggat cagctgctgg 750
tggccgtggc cttaccccaag gccagaagga accagagcca gggcaggaga 800
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tatttcattg actgctggct gctta 2575

<210> 347

<211> 639

<212> PRT

<213> Homo sapiens

<400> 347

Met Leu Leu Arg Lys Arg Tyr Arg His Arg Pro Cys Arg Leu Gln
1 5 10 15

Phe Leu Leu Leu Leu Met Leu Gly Cys Val Leu Met Met Val
20 25 30

Ala Met Leu His Pro Pro His His Thr Leu His Gln Thr Val Thr
35 40 45

Ala Gln Ala Ser Lys His Ser Pro Glu Ala Arg Tyr Arg Leu Asp
50 55 60

Phe Gly Glu Ser Gln Asp Trp Val Leu Glu Ala Glu Asp Glu Gly
65 70 75

Glu Glu Tyr Ser Pro Leu Glu Gly Leu Pro Pro Phe Ile Ser Leu
80 85 90

Arg Glu Asp Gln Leu Leu Val Ala Val Ala Leu Pro Gln Ala Arg
95 100 105

Arg Asn Gln Ser Gln Gly Arg Arg Gly Ser Tyr Arg Leu Ile
110 115 120

Lys Gln Pro Arg Arg Gln Asp Lys Glu Ala Pro Lys Arg Asp Trp
125 130 135

Gly Ala Asp Glu Asp Gly Glu Val Ser Glu Glu Glu Glu Leu Thr
140 145 150

Pro Phe Ser Leu Asp Pro Arg Gly Leu Gln Glu Ala Leu Ser Ala
155 160 165

Arg Ile Pro Leu Gln Arg Ala Leu Pro Glu Val Arg His Pro Leu
170 175 180

Cys Leu Gln Gln His Pro Gln Asp Ser Leu Pro Thr Ala Ser Val
185 190 195

Ile Leu Cys Phe His Asp Glu Ala Trp Ser Thr Leu Leu Arg Thr
200 205 210

Val His Ser Ile Leu Asp Thr Val Pro Arg Ala Phe Leu Lys Glu
215 220 225

Ile Ile Leu Val Asp Asp Leu Ser Gln Gln Gly Gln Leu Lys Ser
230 235 240

Ala Leu Ser Glu Tyr Val Ala Arg Leu Glu Gly Val Lys Leu Leu
245 250 255

Arg Ser Asn Lys Arg Leu Gly Ala Ile Arg Ala Arg Met Leu Gly
 260 265 270
 Ala Thr Arg Ala Thr Gly Asp Val Leu Val Phe Met Asp Ala His
 275 280 285
 Cys Glu Cys His Pro Gly Trp Leu Glu Pro Leu Leu Ser Arg Ile
 290 295 300
 Ala Gly Asp Arg Ser Arg Val Val Ser Pro Val Ile Asp Val Ile
 305 310 315
 Asp Trp Lys Thr Phe Gln Tyr Tyr Pro Ser Lys Asp Leu Gln Arg
 320 325 330
 Gly Val Leu Asp Trp Lys Leu Asp Phe His Trp Glu Pro Leu Pro
 335 340 345
 Glu His Val Arg Lys Ala Leu Gln Ser Pro Ile Ser Pro Ile Arg
 350 355 360
 Ser Pro Val Val Pro Gly Glu Val Val Ala Met Asp Arg His Tyr
 365 370 375
 Phe Gln Asn Thr Gly Ala Tyr Asp Ser Leu Met Ser Leu Arg Gly
 380 385 390
 Gly Glu Asn Leu Glu Leu Ser Phe Lys Ala Trp Leu Cys Gly Gly
 395 400 405
 Ser Val Glu Ile Leu Pro Cys Ser Arg Val Gly His Ile Tyr Gln
 410 415 420
 Asn Gln Asp Ser His Ser Pro Leu Asp Gln Glu Ala Thr Leu Arg
 425 430 435
 Asn Arg Val Arg Ile Ala Glu Thr Trp Leu Gly Ser Phe Lys Glu
 440 445 450
 Thr Phe Tyr Lys His Ser Pro Glu Ala Phe Ser Leu Ser Lys Ala
 455 460 465
 Glu Lys Pro Asp Cys Met Glu Arg Leu Gln Leu Gln Arg Arg Leu
 470 475 480
 Gly Cys Arg Thr Phe His Trp Phe Leu Ala Asn Val Tyr Pro Glu
 485 490 495
 Leu Tyr Pro Ser Glu Pro Arg Pro Ser Phe Ser Gly Lys Leu His
 500 505 510
 Asn Thr Gly Leu Gly Leu Cys Ala Asp Cys Gln Ala Glu Gly Asp
 515 520 525
 Ile Leu Gly Cys Pro Met Val Leu Ala Pro Cys Ser Asp Ser Arg
 530 535 540
 Gln Gln Gln Tyr Leu Gln His Thr Ser Arg Lys Glu Ile His Phe

545	550	555
Gly Ser Pro Gln His Leu Cys Phe Ala Val Arg Gln Glu Gln Val		
560	565	570
Ile Leu Gln Asn Cys Thr Glu Glu Gly Leu Ala Ile His Gln Gln		
575	580	585
His Trp Asp Phe Gln Glu Asn Gly Met Ile Val His Ile Leu Ser		
590	595	600
Gly Lys Cys Met Glu Ala Val Val Gln Glu Asn Asn Lys Asp Leu		
605	610	615
Tyr Leu Arg Pro Cys Asp Gly Lys Ala Arg Gln Gln Trp Arg Phe		
620	625	630
Asp Gln Ile Asn Ala Val Asp Glu Arg		
635		

<210> 348

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 348

ggagaggtgg tggccatgg aag 23

<210> 349

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 349

ctgtcactgc aaggagccaa cacc 24

<210> 350

<211> 45

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-45

<223> Synthetic construct.

<400> 350

tatgtcgctg cgaggtggtg aaaacctcga actgtcttgc aaggc 45

<210> 351
<211> 2524
<212> DNA
<213> Homo sapiens

<400> 351
cgccaagcat gcagtaaagg ctgaaaatct gggtcacagc tgaggaagac 50
ctcagacatg gagtccagga tgtggcctgc gctgctgctg tcccacacctc 100
tccctctctg gccactgctg ttgctgcccc tcccaccgccc tgctcagggc 150
tcttcatcct cccctcgaac cccaccagcc ccagcccgcc ccccggtgtc 200
caggggagggc ccctcggccc cacgtcatgt gtgcgtgtgg gagcgagcac 250
ctccaccaag ccgatctcct cgggtcccaa gatcacgtcg gcaagtccctg 300
cctggcactg caccggcagc caccggcatca ggcttgagg aggggcccgc 350
ctcatcccaa tacccttggg ctatcgtgtg gggtcccacc gtgtctcgag 400
aggatggagg ggaccccaac tctgccaatc ccggatttct ggactatgg 450
tttgcagccc ctcatgggct cgcaacccca caccggact cagactccat 500
gcgaggtgat ggagatgggc ttatccttgg agaggcacct gcccacccctgc 550
ggccattcct gttccccccgc cgtggggaaag gtgtggaccc ccagctctat 600
gtcacaatta ccatctccat catcattgtt ctcgtggcca ctggcatcat 650
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tcaaataaaag ctttgcaag ataa 2524

<210> 352
<211> 243
<212> PRT
<213> Homo sapiens

<400> 352
Met Arg Pro Gln Gly Pro Ala Ala Ser Pro Gln Arg Leu Arg Gly
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Leu Leu Leu Leu Leu Leu Gln Leu Pro Ala Pro Ser Ser Ala
 20 25 30

Ser Glu Ile Pro Lys Gly Lys Gln Lys Ala Gln Leu Arg Gln Arg
 35 40 45

Glu Val Val Asp Leu Tyr Asn Gly Met Cys Leu Gln Gly Pro Ala
 50 55 60

Gly Val Pro Gly Arg Asp Gly Ser Pro Gly Ala Asn Val Ile Pro
 65 70 75

Gly Thr Pro Gly Ile Pro Gly Arg Asp Gly Phe Lys Gly Glu Lys
 80 85 90

Gly Glu Cys Leu Arg Glu Ser Phe Glu Glu Ser Trp Thr Pro Asn
 95 100 105

Tyr Lys Gln Cys Ser Trp Ser Ser Leu Asn Tyr Gly Ile Asp Leu
 110 115 120

Gly Lys Ile Ala Glu Cys Thr Phe Thr Lys Met Arg Ser Asn Ser
 125 130 135

Ala Leu Arg Val Leu Phe Ser Gly Ser Leu Arg Leu Lys Cys Arg
 140 145 150

Asn Ala Cys Cys Gln Arg Trp Tyr Phe Thr Phe Asn Gly Ala Glu
 155 160 165

Cys Ser Gly Pro Leu Pro Ile Glu Ala Ile Ile Tyr Leu Asp Gln
 170 175 180

Gly Ser Pro Glu Met Asn Ser Thr Ile Asn Ile His Arg Thr Ser
 185 190 195

Ser Val Glu Gly Leu Cys Glu Gly Ile Gly Ala Gly Leu Val Asp
 200 205 210

Val Ala Ile Trp Val Gly Thr Cys Ser Asp Tyr Pro Lys Gly Asp
 215 220 225

Ala Ser Thr Gly Trp Asn Ser Val Ser Arg Ile Ile Ile Glu Glu
 230 235 240

Leu Pro Lys

<210> 353
 <211> 480
 <212> DNA
 <213> Homo sapiens

<400> 353
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 cggccaggat ggcattcctgt ctggccctgc gcatggcgct gctgctggtc 100

tccggggttc tggccctgc ggtgctcaca gacgatgttc cacaggagcc 150
cgtccccacg ctgtggaacg agccggccga gctgccgtcg ggagaaggcc 200
ccgtggagag caccagcccc ggccgggagc ccgtggacac cggccccca 250
gccccccacgg tcgcgccagg acccgaggac agcaccgcgc aggagcgct 300
ggaccagggc ggcgggtcgc tggggcccg cgctatcgcg gccatcgta 350
tcgcccgcct gctggccacc tgctgtgtgc tggcgctcg ggtcgctcg 400
ctgagaaagt tttctgcctc ctgaagcgaa taaaggggcc gcgcccggcc 450
gcggcgcgac tcggcaaaaa aaaaaaaaaa 480

<210> 354

<211> 121

<212> PRT

<213> Homo sapiens

<400> 354

Met Ala Ser Cys Leu Ala Leu Arg Met Ala Leu Leu Leu Val Ser
1 5 10 15

Gly Val Leu Ala Pro Ala Val Leu Thr Asp Asp Val Pro Gln Glu
20 25 30

Pro Val Pro Thr Leu Trp Asn Glu Pro Ala Glu Leu Pro Ser Gly
35 40 45

Glu Gly Pro Val Glu Ser Thr Ser Pro Gly Arg Glu Pro Val Asp
50 55 60

Thr Gly Pro Pro Ala Pro Thr Val Ala Pro Gly Pro Glu Asp Ser
65 70 75

Thr Ala Gln Glu Arg Leu Asp Gln Gly Gly Ser Leu Gly Pro
80 85 90

Gly Ala Ile Ala Ala Ile Val Ile Ala Ala Leu Leu Ala Thr Cys
95 100 105

Val Val Leu Ala Leu Val Val Val Ala Leu Arg Lys Phe Ser Ala
110 115 120

Ser

<210> 355

<211> 2134

<212> DNA

<213> Homo sapiens

<400> 355

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gttggccggc ggcggggccgg gacgggcatg gccctgctgc tgcgtcggt 100

gtgcctgacg gcggcgctgg cccacggctg tctgcactgc cacagcaact 150
tctccaagaa gttctcccttc taccgccacc atgtgaactt caagtcctgg 200
tgggtggcg acatccccgt gtcagggcg ctgctcacccg actggagcga 250
cgacacgatg aaggagctgc acctggccat ccccgccaag atcacccggg 300
agaagctgga ccaagtggcg acagcagtgt accagatgtat ggatcagctg 350
taccagggga agatgtactt ccccggtat ttccccaacg agctgcgaaa 400
catcttcccg gaggcagggtgc acctcatcca gaacgccatc atcgaaaggc 450
acctggcacc aggcaagctgg ggaggagggc agctctccag ggagggaccc 500
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tgctccatct cacgctgggg gtcaacctgg ggacccttc cctccgggcc 650
atggacacac atacatgaaa accaggccgc atcgactgtc agcaccgctg 700
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ccatggagggg gctgactgcc ccacattgcc tttcagacag gacacgagca 1350
tgaggttaagg ccgcctgac ctggacttca gggggagggg gtaaaggag 1400
agaggagggg ggcttaggggg tcctcttagat cagtgggggc actgcaggtg 1450
gggctctccc tataccctggg acacctgctg gatgtcacct ctgcaaccac 1500
acccatgtgg tggtttcatg aacagaccac gctcctctgc cttctcctgg 1550

cctgggacac acagagccac cccggccttg tgagtgaccc agagaaggga 1600
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gctggcctg ccccaggca acgtggggc ggagactcag ctggacagcc 1950
cctgcctgtc actctggagc tgggctgctg ctgcctcagg accccctctc 2000
cgaccccgga cagagctgag ctggccaggg ccaggagggc gggagggagg 2050
gaatgggggt gggctgtgcg cagcatcagc gcctggcagag gtccgcagag 2100
ctgcggatg tgattaaagt ccctgatgtt tctc 2134

<210> 356

<211> 157

<212> PRT

<213> Homo sapiens

<400> 356

Met	Ala	Leu	Leu	Leu	Cys	Leu	Val	Cys	Leu	Thr	Ala	Ala	Leu	Ala
1					5				10					15
His	Gly	Cys	Leu	His	Cys	His	Ser	Asn	Phe	Ser	Lys	Lys	Phe	Ser
						20				25				30
Phe	Tyr	Arg	His	His	Val	Asn	Phe	Lys	Ser	Trp	Trp	Val	Gly	Asp
					35				40					45
Ile	Pro	Val	Ser	Gly	Ala	Leu	Leu	Thr	Asp	Trp	Ser	Asp	Asp	Thr
					50				55					60
Met	Lys	Glu	Leu	His	Leu	Ala	Ile	Pro	Ala	Lys	Ile	Thr	Arg	Glu
					65				70					75
Lys	Leu	Asp	Gln	Val	Ala	Thr	Ala	Val	Tyr	Gln	Met	Met	Asp	Gln
					80				85					90
Leu	Tyr	Gln	Gly	Lys	Met	Tyr	Phe	Pro	Gly	Tyr	Phe	Pro	Asn	Glu
					95				100					105
Leu	Arg	Asn	Ile	Phe	Arg	Glu	Gln	Val	His	Leu	Ile	Gln	Asn	Ala
					110				115					120
Ile	Ile	Glu	Arg	His	Leu	Ala	Pro	Gly	Ser	Trp	Gly	Gly	Gly	Gln
					125				130					135
Leu	Ser	Arg	Glu	Gly	Pro	Ser	Leu	Ala	Pro	Glu	Gly	Ser	Met	Pro

140

145

150

Ser Pro Arg Gly Asp Leu Pro
155

<210> 357

<211> 1536

<212> DNA

<213> Homo sapiens

<400> 357

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cctcttattt ctcctcacgt gtgagctggc tgcagaagtt gctgcagaag 100
ttgagaaatc ctcagatggt cctggtgctg cccaggaacc cacgtggctc 150
acagatgtcc cagctgccat ggaattcatt gctgccactg aggtggctgt 200
cataggcttc ttccaggatt tagaaatacc agcagtgcac atactccata 250
gcatggtgca aaaattccca ggcgtgtcat ttgggatcag cactgattct 300
gaggttctga cacactacaa catcaactggg aacaccatct gcctcttcg 350
cctggtagac aatgaacaac tgaattttaga ggacgaagac attgaaagca 400
ttgatgccac caaattgagc cgtttcattt agatcaacag cctccacatg 450
gtgacagagt acaaccctgt gactgtgatt gggttattca acagcgtaat 500
tcagattcat ctcctcctga taatgaacaa ggctccccca gagttatgaa 550
agaacatgca cagataccag aaggcagcca agctcttcca ggggaagatt 600
ctctttattt tggggacag tggatgaaa gaaaatggga aggtgatatac 650
attttcaaa ctaaaggagt ctcaactgccc agctttggca atttaccaga 700
ctcttagatga cgagtggat acactgccc cagcagaagt ttccgttagag 750
catgtgcaaa acttttgta tggattccta agtggaaaat tggatgaaaga 800
aaatcgtgaa tcagaaggaa agactccaaa ggtggaaactc tgacttctcc 850
ttggaaactac atatggccaa gtatctactt tatgcaaagt aaaaaggcac 900
aactcaaattc tcagagacac taaacaacag gatcaacttgg cctgccaacc 950
acacacacac gcacgtgcac acacgcacgc acgcgtgcac acacacacgc 1000
gcacacacac acacacacag agcttcattt cctgtcttaa aatctcggtt 1050
tctcttccttc cttcttttaa atttcatatc ctcactccct atccaatttc 1100
cttcttatacg tgcattcata ctctgtaaac ccattctgtaa cacacctaga 1150
tcaaggcttt aagagactca ctgtgatgcc tctatgaaag agaggcattc 1200

ctagagaaag attgttccaa tttgtcattt aatatcaagt ttgtatactg 1250
cacatgactt acacacaaca tagttcctgc tcttttaagg ttacctaagg 1300
gttgaaactc taccttcttt cataaggaca tgtccgtctc tgactcagga 1350
tcaaaaacca aaggatggtt ttaaacacct ttgtgaaatt gtcttttgc 1400
cagaagttaa aggctgtctc caagtccctg aactcagcag aaatagacca 1450
tgtgaaaact ccatgcttgg ttagcatctc caactcccta tgtaaatcaa 1500
caacctgcat aataaataaa aggcaatcat gttata 1536

<210> 358

<211> 273

<212> PRT

<213> Homo sapiens

<400> 358

Met Glu Ala Ala Pro Ser Arg Phe Met Phe Leu Leu Phe Leu Leu
1 5 10 15

Thr Cys Glu Leu Ala Ala Glu Val Ala Ala Glu Val Glu Lys Ser
20 25 30

Ser Asp Gly Pro Gly Ala Ala Gln Glu Pro Thr Trp Leu Thr Asp
35 40 45

Val Pro Ala Ala Met Glu Phe Ile Ala Ala Thr Glu Val Ala Val
50 55 60

Ile Gly Phe Phe Gln Asp Leu Glu Ile Pro Ala Val Pro Ile Leu
65 70 75

His Ser Met Val Gln Lys Phe Pro Gly Val Ser Phe Gly Ile Ser
80 85 90

Thr Asp Ser Glu Val Leu Thr His Tyr Asn Ile Thr Gly Asn Thr
95 100 105

Ile Cys Leu Phe Arg Leu Val Asp Asn Glu Gln Leu Asn Leu Glu
110 115 120

Asp Glu Asp Ile Glu Ser Ile Asp Ala Thr Lys Leu Ser Arg Phe
125 130 135

Ile Glu Ile Asn Ser Leu His Met Val Thr Glu Tyr Asn Pro Val
140 145 150

Thr Val Ile Gly Leu Phe Asn Ser Val Ile Gln Ile His Leu Leu
155 160 165

Leu Ile Met Asn Lys Ala Ser Pro Glu Tyr Glu Glu Asn Met His
170 175 180

Arg Tyr Gln Lys Ala Ala Lys Leu Phe Gln Gly Lys Ile Leu Phe
185 190 195

Ile Leu Val Asp Ser Gly Met Lys Glu Asn Gly Lys Val Ile Ser
200 205 210
Phe Phe Lys Leu Lys Glu Ser Gln Leu Pro Ala Leu Ala Ile Tyr
215 220 225
Gln Thr Leu Asp Asp Glu Trp Asp Thr Leu Pro Thr Ala Glu Val
230 235 240
Ser Val Glu His Val Gln Asn Phe Cys Asp Gly Phe Leu Ser Gly
245 250 255
Lys Leu Leu Lys Glu Asn Arg Glu Ser Glu Gly Lys Thr Pro Lys
260 265 270
Val Glu Leu

<210> 359

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 359

ccagcagtgc ccatactcca tagc 24

<210> 360

<211> 20

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-20

<223> Synthetic construct.

<400> 360

tgacgagttgg gatacactgc 20

<210> 361

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 361

gctctacgga aacttctgct gtgg 24

<210> 362

<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 362
attcccaggc gtgtcatttggatcagcac tgattcttagtctgacac 50

<210> 363
<211> 1777
<212> DNA
<213> Homo sapiens

<400> 363
ggagagccgc ggctgggacc ggagtgggaa ggcggcggtg gaggtgcac 50
ccggcgcggg tggcgagag atcagaagcc tcttcccaa gcccggccaa 100
cctcagcggg gaccgggct cagggacgcg ggcggcggtg cggcgactgc 150
agtggctgga cgatggcagc gtccggccgaa gcccggggtg tgattgcagc 200
cccagacagc cggcgctggc tgtggcggt gctggcggtg ggcgttggc 250
tcttgcacagc tggagtatca gccttggaaatatacggcc aaaagaaatc 300
ttcgtggcaa atggacaca agggaaatgc acctgcaatg tcaagtctac 350
tagtacgact ggcgggttga cctcagtcctc ctggagcttc cagccagagg 400
ggccgacac tactgtgtcg ttttccact actcccaagg gcaagtgtac 450
cttggaaatt atccaccatt taaagacaga atcagctggg ctggagacct 500
tgacaagaaa gatgcataa tcaacataga aaatatgcag tttatacaca 550
atggcaccta tatctgtat gtcaaaaacc ctcctgacat cttgtccag 600
cctggacaca ttaggctcta tgctgttagaa aaagagaatt tgctgtgtt 650
tccagtttgg gtagtggtagtgcatagttac tgctgtgtc ctaggtctca 700
ctctgctcat cagcatgatt ctggctgtcc tctatagaag gaaaaactct 750
aaacgggatt acactggctg cagtagatca gagagttgt caccagttaa 800
gcaggctcct cggaaatccc ctcggacac tgagggtttt gtaaagagtc 850
tgccttctgg atctcaccag ggcccagtca tataatgcaca gtttagaccac 900
tccggcggac atcacagtga caagattaac aagtcaatgt ctgtgggtgt 950
tgcggatatac cgaaagaatt aagagaatac ctggaaacata tcctcagcaa 1000

gaaacaaaac caaactggac tctcgtgcag aaaatgtgc ccattaccac 1050
atgtgcctt ggagacccag gcaaggacaa gtacacgtgt actcacagag 1100
ggagagaaag atgtgtacaa aggatatgt aaaaatattct attttgtcat 1150
cctgatatga ggagccagtg ttgcattatg aaaagatggt atgattctac 1200
atatgtaccc attgtttgc tggtttgtt ctttctttc aggtcattta 1250
caattggag atttcagaaa catttcatttc accatcattt agaaatggtt 1300
tgcccttaatg gagacaatag cagatcctgt agtatttcca gtagacatgg 1350
ccttttaatc taaggccta agactgatta gtcttagcat ttactgttagt 1400
tggaggatgg agatgctatg atgaaagcat acccagggtg gccttagca 1450
cagtatcgtt accattttt tgtctgcgc tttaaaaaa tacccattgg 1500
ctatgccact tgaaaacaat ttgagaagtt ttttgaagt ttttctact 1550
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tttgcaccc taaaatgtgt catatcaatt tctggattca taatagcaag 1650
attagcaaag gataaatgcc gaaggtcaat tcattctgga cacagttgga 1700
tcaataactga ttaagtagaa aatccaagct ttgcttgaga actttttaaa 1750
cgtggagagt aaaaagtatc ggtttta 1777

<210> 364

<211> 269

<212> PRT

<213> Homo sapiens

<400> 364

Met	Ala	Ala	Ser	Ala	Gly	Ala	Gly	Ala	Val	Ile	Ala	Ala	Pro	Asp
1									10				15	
Ser	Arg	Arg	Trp	Leu	Trp	Ser	Val	Leu	Ala	Ala	Ala	Leu	Gly	Leu
									25				30	
Leu	Thr	Ala	Gly	Val	Ser	Ala	Leu	Glu	Val	Tyr	Thr	Pro	Lys	Glu
									40				45	
Ile	Phe	Val	Ala	Asn	Gly	Thr	Gln	Gly	Lys	Leu	Thr	Cys	Lys	Phe
									55				60	
Lys	Ser	Thr	Ser	Thr	Thr	Gly	Gly	Leu	Thr	Ser	Val	Ser	Trp	Ser
									65				75	
Phe	Gln	Pro	Glu	Gly	Ala	Asp	Thr	Thr	Val	Ser	Phe	Phe	His	Tyr
									80				90	
Ser	Gln	Gly	Gln	Val	Tyr	Leu	Gly	Asn	Tyr	Pro	Pro	Phe	Lys	Asp
									95				105	

Arg Ile Ser Trp Ala Gly Asp Leu Asp Lys Lys Asp Ala Ser Ile
 110 115 120
 Asn Ile Glu Asn Met Gln Phe Ile His Asn Gly Thr Tyr Ile Cys
 125 130 135
 Asp Val Lys Asn Pro Pro Asp Ile Val Val Gln Pro Gly His Ile
 140 145 150
 Arg Leu Tyr Val Val Glu Lys Glu Asn Leu Pro Val Phe Pro Val
 155 160 165
 Trp Val Val Val Gly Ile Val Thr Ala Val Val Leu Gly Leu Thr
 170 175 180
 Leu Leu Ile Ser Met Ile Leu Ala Val Leu Tyr Arg Arg Lys Asn
 185 190 195
 Ser Lys Arg Asp Tyr Thr Gly Cys Ser Thr Ser Glu Ser Leu Ser
 200 205 210
 Pro Val Lys Gln Ala Pro Arg Lys Ser Pro Ser Asp Thr Glu Gly
 215 220 225
 Leu Val Lys Ser Leu Pro Ser Gly Ser His Gln Gly Pro Val Ile
 230 235 240
 Tyr Ala Gln Leu Asp His Ser Gly Gly His His Ser Asp Lys Ile
 245 250 255
 Asn Lys Ser Glu Ser Val Val Tyr Ala Asp Ile Arg Lys Asn
 260 265

<210> 365
 <211> 1321
 <212> DNA
 <213> Homo sapiens

<400> 365
 gccggctgtg cagagacgcc atgtaccggc tcctgtcagc agtgactgcc 50
 cgggctgccg ccccccgggg cttggcctca agctgcggac gacgcggggt 100
 ccatcagcgc gccgggctgc cgcctctcgg ccacggctgg gtcgggggcc 150
 tcgggctggg gctggggctg gcgctcgggg tgaagctggc aggtgggctg 200
 aggggcgcgg ccccgccgca gtcccccgcg gcccccgacc ctgaggcgac 250
 gcctctggcc gagccgccac aggagcagtc cctcgccccc tggtctccgc 300
 agaccccgac gccgcctgc tccaggtgt tcggccagagc catcgagagc 350
 agccgcgacc tgctgcacag gatcaaggat gaggtggcgc caccggcat 400
 agtggttgga gtttctgttag atggaaaaga agtctggtca gaaggtttag 450
 gttatgctga tggatggaaac cgtgttaccat gtaaaccaga gacagttatg 500

cgaattgcta gcatcagcaa aagtctcacc atggggcgtc ttgccaaatt 550
gtggaaagca gggaaactgg atcttgatat tccagtacaa cattatgttc 600
ccgaattccc agaaaaagaa tatgaagggtg aaaagggttc tgtcacaaca 650
agattactga tttcccatat aagtggatt cgtcattatg aaaaggacat 700
aaaaaaagggtg aaagaagaga aagcttataa agccttgaag atgatgaaag 750
agaatgtgc atttgagcaa gaaaaagaag gcaaaaagtaa tgaaaagaat 800
gattttacta aatttaaaac agagcaggag aatgaagcca aatgccgaa 850
ttcaaaaacct ggcaagaaaa agaatgattt tgaacaaggc gaattatatt 900
tgagagaaaa gtttggaaat tcaattgaat ccctaagatt atttaaaaat 950
gatccttgc tcttcaaacc tggtagtcag tttttgtatt caactttgg 1000
ctatacccta ctggcagcca tagtagagag agttcagga tgtaaatatt 1050
tggactatat gcagaaaata ttccatgact tggatatgct gacgactgtg 1100
caggaagaaa acgagccagt gatttacaat agagcaaggt aaatgaatac 1150
cttctgctgt gtctagctat atcgcacatctt aacactatatt tattaattaa 1200
aagtcaaatt ttctttgttt ccattccaaa atcaacctgc cacattttgg 1250
gagctttctt acatgtctgt tttctcatct gtaaagtgaa ggaagtaaaa 1300
catgtttata aagtaaaaaa a 1321

<210> 366

<211> 373

<212> PRT

<213> Homo sapiens

<400> 366

Met	Tyr	Arg	Leu	Leu	Ser	Ala	Val	Thr	Ala	Arg	Ala	Ala	Ala	Pro
1			5				10							15
Gly	Gly	Leu	Ala	Ser	Ser	Cys	Gly	Arg	Arg	Gly	Val	His	Gln	Arg
		20					25							30
Ala	Gly	Leu	Pro	Pro	Leu	Gly	His	Gly	Trp	Val	Gly	Gly	Leu	Gly
		35						40						45
Leu	Gly	Leu	Gly	Leu	Ala	Leu	Gly	Val	Lys	Leu	Ala	Gly	Gly	Leu
		50						55						60
Arg	Gly	Ala	Ala	Pro	Ala	Gln	Ser	Pro	Ala	Ala	Pro	Asp	Pro	Glu
				65				70						75
Ala	Ser	Pro	Leu	Ala	Glu	Pro	Pro	Gln	Glu	Gln	Ser	Leu	Ala	Pro
				80				85						90

Trp Ser Pro Gln Thr Pro Ala Pro Pro Cys Ser Arg Cys Phe Ala
 95 100 105
 Arg Ala Ile Glu Ser Ser Arg Asp Leu Leu His Arg Ile Lys Asp
 110 115 120
 Glu Val Gly Ala Pro Gly Ile Val Val Gly Val Ser Val Asp Gly
 125 130 135
 Lys Glu Val Trp Ser Glu Gly Leu Gly Tyr Ala Asp Val Glu Asn
 140 145 150
 Arg Val Pro Cys Lys Pro Glu Thr Val Met Arg Ile Ala Ser Ile
 155 160 165
 Ser Lys Ser Leu Thr Met Val Ala Leu Ala Lys Leu Trp Glu Ala
 170 175 180
 Gly Lys Leu Asp Leu Asp Ile Pro Val Gln His Tyr Val Pro Glu
 185 190 195
 Phe Pro Glu Lys Glu Tyr Glu Gly Glu Lys Val Ser Val Thr Thr
 200 205 210
 Arg Leu Leu Ile Ser His Leu Ser Gly Ile Arg His Tyr Glu Lys
 215 220 225
 Asp Ile Lys Lys Val Lys Glu Glu Lys Ala Tyr Lys Ala Leu Lys
 230 235 240
 Met Met Lys Glu Asn Val Ala Phe Glu Gln Glu Lys Glu Gly Lys
 245 250 255
 Ser Asn Glu Lys Asn Asp Phe Thr Lys Phe Lys Thr Glu Gln Glu
 260 265 270
 Asn Glu Ala Lys Cys Arg Asn Ser Lys Pro Gly Lys Lys Asn
 275 280 285
 Asp Phe Glu Gln Gly Glu Leu Tyr Leu Arg Glu Lys Phe Glu Asn
 290 295 300
 Ser Ile Glu Ser Leu Arg Leu Phe Lys Asn Asp Pro Leu Phe Phe
 305 310 315
 Lys Pro Gly Ser Gln Phe Leu Tyr Ser Thr Phe Gly Tyr Thr Leu
 320 325 330
 Leu Ala Ala Ile Val Glu Arg Ala Ser Gly Cys Lys Tyr Leu Asp
 335 340 345
 Tyr Met Gln Lys Ile Phe His Asp Leu Asp Met Leu Thr Thr Val
 350 355 360
 Gln Glu Glu Asn Glu Pro Val Ile Tyr Asn Arg Ala Arg
 365 370

<210> 367

<211> 30
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-30
<223> Synthetic construct.

<400> 367
tggaaaagaa gtctggtcag aaggtagg 30

<210> 368
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-25
<223> Synthetic construct.

<400> 368
catttggctt catttcctg ctctg 25

<210> 369
<211> 28
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-28
<223> Synthetic construct.

<400> 369
aaaacctcag aacaactcat tttgcacc 28

<210> 370
<211> 41
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-41
<223> Synthetic construct.

<400> 370
gtctcaccat gggtgcttt gccaaattgt gggaaagg 41

<210> 371
<211> 1150
<212> DNA
<213> Homo sapiens

<400> 371
gtgacactat agaagagcta tgacgtcgca tgcacgcgtc cgtaagctcg 50

gaattcggt cgaggctggt gggagaagc cgagatggcg gcagccagcg 100
ctggggcaac ccggctgctc ctgctcttgc tcatggcggt agcagcgccc 150
agtcgagccc gggcagcgg ctgccggcc gggactggtg cgcgaggggc 200
tggggcgaa ggtcgagagg gcgaggcctg tggcacggtg gggctgctgc 250
tggagcactc attttagatc gatgacagt ccaacttccg gaagcggggc 300
tcactgctct ggaaccagca ggtatggtacc ttgtccctgt cacagcggca 350
gctcagcgag gaggagcggg gccgactccg ggtatgtggca gccctgaatg 400
gcctgtaccg ggtccggatc ccaaggcgac ccggggccct ggtatggcctg 450
gaagctggtg gctatgtctc ctcccttgc cctgcgtgct ccctggtgga 500
gtcgcacccg tcggaccaggc tgaccctgca cgtggatgtg gccggcaacg 550
tggtggcggt gtcgggtggt acgcaccccg ggggctgccc gggccatgag 600
gtggaggacg tggacctgga gctgttcaac acctcggtgc agctgcagcc 650
gcccaccaca gccccaggcc ctgagacggc ggccttcatt gagcgcctgg 700
agatggaaca gccccagaag gccaagaacc cccaggagca gaagtccttc 750
ttcgccaaat actggatgta catcattccc gtcgtccctgt tcctcatgat 800
gtcaggagcg ccagacaccg ggggcccaggg tgggggtggg ggtgggggtg 850
gtggtggggg tagtggcctt tgctgtgtgc caccctccct gtaagtctat 900
ttaaaaacat cgacgataca ttgaaatgtg tgaacgtttt gaaaagctac 950
agcttccagc agccaaaagc aactgttgtt ttggcaagac ggtcctgatg 1000
tacaagcttg attgaaattc actgctact tgatacgtta ttcagaaacc 1050
caaggaatgg ctgtccccat cctcatgtgg ctgtgtggag ctcagctgtg 1100
ttgtgtggca gtttattaaa ctgtccccca gatcgacacg caaaaaaaaaa 1150

<210> 372

<211> 269

<212> PRT

<213> Homo sapiens

<400> 372

Met	Ala	Ala	Ala	Ser	Ala	Gly	Ala	Thr	Arg	Leu	Leu	Leu	Leu	Leu
1					5				10					15

Leu	Met	Ala	Val	Ala	Ala	Pro	Ser	Arg	Ala	Arg	Gly	Ser	Gly	Cys
						20				25				30

Arg	Ala	Gly	Thr	Gly	Ala	Arg	Gly	Ala	Gly	Ala	Glu	Gly	Arg	Glu
					35				40					45

Gly Glu Ala Cys Gly Thr Val Gly Leu Leu Leu Glu His Ser Phe
 50 55 60

Glu Ile Asp Asp Ser Ala Asn Phe Arg Lys Arg Gly Ser Leu Leu
 65 70 75

Trp Asn Gln Gln Asp Gly Thr Leu Ser Leu Ser Gln Arg Gln Leu
 80 85 90

Ser Glu Glu Glu Arg Gly Arg Leu Arg Asp Val Ala Ala Leu Asn
 95 100 105

Gly Leu Tyr Arg Val Arg Ile Pro Arg Arg Pro Gly Ala Leu Asp
 110 115 120

Gly Leu Glu Ala Gly Gly Tyr Val Ser Ser Phe Val Pro Ala Cys
 125 130 135

Ser Leu Val Glu Ser His Leu Ser Asp Gln Leu Thr Leu His Val
 140 145 150

Asp Val Ala Gly Asn Val Val Gly Val Ser Val Val Thr His Pro
 155 160 165

Gly Gly Cys Arg Gly His Glu Val Glu Asp Val Asp Leu Glu Leu
 170 175 180

Phe Asn Thr Ser Val Gln Leu Gln Pro Pro Thr Thr Ala Pro Gly
 185 190 195

Pro Glu Thr Ala Ala Phe Ile Glu Arg Leu Glu Met Glu Gln Ala
 200 205 210

Gln Lys Ala Lys Asn Pro Gln Glu Gln Lys Ser Phe Phe Ala Lys
 215 220 225

Tyr Trp Met Tyr Ile Ile Pro Val Val Leu Phe Leu Met Met Ser
 230 235 240

Gly Ala Pro Asp Thr Gly Gly Gln Gly Gly Gly Gly Gly Gly
 245 250 255

Gly Gly Gly Ser Gly Leu Cys Cys Val Pro Pro Ser Leu
 260 265

<210> 373

<211> 1706

<212> DNA

<213> Homo sapiens

<400> 373

ggagcgctgc tggaacccga gccggagccg gagccacagc ggggagggtg 50

gcctggcggc ctggagccgg acgtgtccgg ggcgtccccg cagaccgggg 100

cagcaggtcg tccgggggccc caccatgtcg gtgactgcct accttgcttt 150

tgttaggcctc ctggcctcct gcctggggct ggaactgtca agatgccggg 200

ctaaaccccc tggaaaggcc tgcagcaatc cctccttcct tcggtttcaa 250
ctggacttct atcaggtcta cttcctggcc ctggcagctg attggcttca 300
ggcccccctac ctctataaac tctaccagca ttactacttc ctggaaggtc 350
aaattgccat cctctatgtc tgtggccttg cctctacagt cctctttggc 400
ctagtggcct cctcccttgt ggattggctg ggtcgcaaga attcttgtgt 450
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actacttgt gctgctagt gggcgagcac ttggggcgt gtccacagcc 550
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gcatgacttc cctgctgagt ggatcccagc taccttgct cgagctgcct 650
tctggAACCA tgtgctggct gtagtggcag gtgtggcagc tgaggctgta 700
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tctcctggct ctggcagggg ccttggccct tcgaaactgg ggggagaact 800
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cacacggggc ccctctgggc attatcttct ccagcttcat ggcagccagc 1000
ctgcttggct cttccctgta ccgtatcgcc acctccaaga ggtaccacct 1050
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tcttcatgtt gacttctct accagcccg gccaggagag tccgggtggag 1150
tccttcatacg cttttctact tattgagttg gcttggat tatactttcc 1200
cagcatgagc ttcctacgga gaaagggtat ccctgagaca gagcaggctg 1250
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gggacagact cttgaattcc agctatccgg gattgtacag atctctctgt 1550
gactgacttt gtgactgtcc tgtggttctt cctgccattt ctttgtttt 1600
gggaggacat gatgggggtg atggactgga aagaaggtgc caaaagtcc 1650

ctctgtgtta ctcccatat aaaaataaac actttaaat gatcaaaaaa 1700
aaaaaa 1706

<210> 374
<211> 450
<212> PRT
<213> Homo sapiens

<400> 374

Met	Leu	Val	Thr	Ala	Tyr	Leu	Ala	Phe	Val	Gly	Leu	Leu	Ala	Ser
1					5				10					15
Cys	Leu	Gly	Leu	Glu	Leu	Ser	Arg	Cys	Arg	Ala	Lys	Pro	Pro	Gly
	20						25							30
Arg	Ala	Cys	Ser	Asn	Pro	Ser	Phe	Leu	Arg	Phe	Gln	Leu	Asp	Phe
	35							40						45
Tyr	Gln	Val	Tyr	Phe	Leu	Ala	Leu	Ala	Asp	Trp	Leu	Gln	Ala	
	50						55						60	
Pro	Tyr	Leu	Tyr	Lys	Leu	Tyr	Gln	His	Tyr	Tyr	Phe	Leu	Glu	Gly
	65						70						75	
Gln	Ile	Ala	Ile	Leu	Tyr	Val	Cys	Gly	Leu	Ala	Ser	Thr	Val	Leu
	80							85					90	
Phe	Gly	Leu	Val	Ala	Ser	Ser	Leu	Val	Asp	Trp	Leu	Gly	Arg	Lys
	95							100					105	
Asn	Ser	Cys	Val	Leu	Phe	Ser	Leu	Thr	Tyr	Ser	Leu	Cys	Cys	Leu
	110							115					120	
Thr	Lys	Leu	Ser	Gln	Asp	Tyr	Phe	Val	Leu	Leu	Val	Gly	Arg	Ala
	125							130					135	
Leu	Gly	Gly	Leu	Ser	Thr	Ala	Leu	Leu	Phe	Ser	Ala	Phe	Glu	Ala
	140							145					150	
Trp	Tyr	Ile	His	Glu	His	Val	Glu	Arg	His	Asp	Phe	Pro	Ala	Glu
	155							160	"				165	
Trp	Ile	Pro	Ala	Thr	Phe	Ala	Arg	Ala	Ala	Phe	Trp	Asn	His	Val
	170							175					180	
Leu	Ala	Val	Val	Ala	Gly	Val	Ala	Ala	Glu	Ala	Val	Ala	Ser	Trp
	185							190					195	
Ile	Gly	Leu	Gly	Pro	Val	Ala	Pro	Phe	Val	Ala	Ala	Ile	Pro	Leu
	200							205					210	
Leu	Ala	Leu	Ala	Gly	Ala	Leu	Ala	Leu	Arg	Asn	Trp	Gly	Glu	Asn
	215							220					225	
Tyr	Asp	Arg	Gln	Arg	Ala	Phe	Ser	Arg	Thr	Cys	Ala	Gly	Gly	Leu
	230							235					240	

Arg	Cys	Leu	Leu	Ser	Asp	Arg	Arg	Val	Leu	Leu	Leu	Gly	Thr	Ile
									245	250	250			255
Gln	Ala	Leu	Phe	Glu	Ser	Val	Ile	Phe	Ile	Phe	Val	Phe	Leu	Trp
									260	265	265			270
Thr	Pro	Val	Leu	Asp	Pro	His	Gly	Ala	Pro	Leu	Gly	Ile	Ile	Phe
									275	280	280			285
Ser	Ser	Phe	Met	Ala	Ala	Ser	Leu	Leu	Gly	Ser	Ser	Leu	Tyr	Arg
									290	295	295			300
Ile	Ala	Thr	Ser	Lys	Arg	Tyr	His	Leu	Gln	Pro	Met	His	Leu	Leu
									305	310	310			315
Ser	Leu	Ala	Val	Leu	Ile	Val	Val	Phe	Ser	Leu	Phe	Met	Leu	Thr
									320	325	325			330
Phe	Ser	Thr	Ser	Pro	Gly	Gln	Glu	Ser	Pro	Val	Glu	Ser	Phe	Ile
									335	340	340			345
Ala	Phe	Leu	Leu	Ile	Glu	Leu	Ala	Cys	Gly	Leu	Tyr	Phe	Pro	Ser
									350	355	355			360
Met	Ser	Phe	Leu	Arg	Arg	Lys	Val	Ile	Pro	Glu	Thr	Glu	Gln	Ala
									365	370	370			375
Gly	Val	Leu	Asn	Trp	Phe	Arg	Val	Pro	Leu	His	Ser	Leu	Ala	Cys
									380	385	385			390
Leu	Gly	Leu	Leu	Val	Leu	His	Asp	Ser	Asp	Arg	Lys	Thr	Gly	Thr
									395	400	400			405
Arg	Asn	Met	Phe	Ser	Ile	Cys	Ser	Ala	Val	Met	Val	Met	Ala	Leu
									410	415	415			420
Leu	Ala	Val	Val	Gly	Leu	Phe	Thr	Val	Val	Arg	His	Asp	Ala	Glu
									425	430	430			435
Leu	Arg	Val	Pro	Ser	Pro	Thr	Glu	Glu	Pro	Tyr	Ala	Pro	Glu	Leu
									440	445	445			450
<210> 375														
<211> 1098														
<212> DNA														
<213> Artificial														
<400> 375														
gcgacgcgcg gcggggcggc gagagaaac gcggcgccgg gcccggcccg 50														
gcccggaga tggtccccgg cgccgcggc tggtgtgtc tcgtgctctg 100														
gctccccgcg tgcgtcgcgg cccacggctt ccgtatccat gattattgt 150														
actttcaagt gctgagtccct ggggacatTC gatacatctt cacagccaca 200														
cctgccaagg actttggtggtt tatctttcac acaaggtatg agcagattca 250														

ccttgtcccc gctgaacctc cagaggcctg cggggactc agcaacggtt 300
tcttcatcca ggaccagatt gctctggtgg agaggggggg ctgctcccttc 350
ctctccaaga ctcgggtggt ccaggagcac ggcgggcggg cggtgatcat 400
ctctgacaac gcagttgaca atgacagctt ctacgtggag atgatccagg 450
acagtaccca ggcacagact gacatccccg ccctttcct gctggccga 500
gacggctaca tgatccgccc ctctctggaa cagcatggc tgccatggc 550
catcatttcc atcccagtca atgtcaccag catccccacc tttgagctgc 600
tgcaaccgcc ctggaccccttc tggtagaaga gtttgcctca cattccagcc 650
ataagtgact ctgagctggg aaggggaaac ccaggaattt tgctacttgg 700
aatttggaga tagcatctgg ggacaagtgg agccaggtag aggaaaagg 750
tttggcggt gctaggctga aagggaagcc acaccactgg cttcccttc 800
cccaggccc ccaagggtgt ctcatgctac aagaagaggc aagagacagg 850
ccccaggcgt tctggctaga acccgaaaca aaaggagctg aaggcaggtg 900
gcctgagagc catctgtgac ctgtcacact cacctggctc cagcctcccc 950
tacccagggt ctctgcacag tgaccttcac agcagttgtt ggagtggttt 1000
aaagagctgg tgtttggga ctcaataaac cctcaactgac ttttagcaa 1050
taaagcttct catcagggtt gcaaaaaaaaaaaaaaaaaaaaaaaa 1098

<210> 376

<211> 188

<212> PRT

<213> Homo sapiens

<400> 376

Met	Val	Pro	Gly	Ala	Ala	Gly	Trp	Cys	Cys	Leu	Val	Leu	Trp	Leu
1										10	"			15

Pro	Ala	Cys	Val	Ala	Ala	His	Gly	Phe	Arg	Ile	His	Asp	Tyr	Leu
										20	25			30

Tyr	Phe	Gln	Val	Leu	Ser	Pro	Gly	Asp	Ile	Arg	Tyr	Ile	Phe	Thr
									35	40				45

Ala	Thr	Pro	Ala	Lys	Asp	Phe	Gly	Ile	Phe	His	Thr	Arg	Tyr	
									50	55				60

Glu	Gln	Ile	His	Leu	Val	Pro	Ala	Glu	Pro	Pro	Glu	Ala	Cys	Gly
									65	70				75

Glu	Leu	Ser	Asn	Gly	Phe	Phe	Ile	Gln	Asp	Gln	Ile	Ala	Leu	Val
									80	85				90

Glu Arg Gly Gly Cys Ser Phe Leu Ser Lys Thr Arg Val Val Gln
95 100 105
Glu His Gly Gly Arg Ala Val Ile Ile Ser Asp Asn Ala Val Asp
110 115 120
Asn Asp Ser Phe Tyr Val Glu Met Ile Gln Asp Ser Thr Gln Arg
125 130 135
Thr Ala Asp Ile Pro Ala Leu Phe Leu Leu Gly Arg Asp Gly Tyr
140 145 150
Met Ile Arg Arg Ser Leu Glu Gln His Gly Leu Pro Trp Ala Ile
155 160 165
Ile Ser Ile Pro Val Asn Val Thr Ser Ile Pro Thr Phe Glu Leu
170 175 180
Leu Gln Pro Pro Trp Thr Phe Trp
185

<210> 377
<211> 496
<212> DNA
<213> Artificial

<220>
<221> unsure
<222> 396
<223> unknown base

<400> 377
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ggctgggt gatggctgggt gtgattccaa tccagggcgg gatcctgaac 100
ctgaacaaga tggtaagca agtgactggg aaaatgccc a tccctcccta 150
ctggccctac ggctgtcact gcggacttagg tggcagagggc caacccaaag 200
atgccacgga ctggtgctgc cagacccatg actgctgcta tgaccacctg 250
aagacccagg ggtgcggcat ctacaaggac aacaacaaaa gcagcataca 300
ttgtatggat ttatctcaac gctattgtt aatggctgtg ttatgtga 350
tctatctgga aatgaggac tccgaataaa aagctattac tawtnaaaa 400
aaaaaaaaaaa aaaaaaaaaaa aaaaaaaaaaa aaaaaaaaaaa aaaaaaaaaaa 450
aaaaaaaaaaa aaaaaaaaaaa aaaaaaaaaaa aaaaaaaaaaa aaaaaaa 496

<210> 378
<211> 116
<212> PRT
<213> Homo sapiens

<400> 378

Met Glu Leu Ala Leu Leu Cys Gly Leu Val Val Met Ala Gly Val
1 5 10 15

Ile Pro Ile Gln Gly Gly Ile Leu Asn Leu Asn Lys Met Val Lys
20 25 30

Gln Val Thr Gly Lys Met Pro Ile Leu Ser Tyr Trp Pro Tyr Gly
35 40 45

Cys His Cys Gly Leu Gly Gly Arg Gly Gln Pro Lys Asp Ala Thr
50 55 60

Asp Trp Cys Cys Gln Thr His Asp Cys Cys Tyr Asp His Leu Lys
65 70 75

Thr Gln Gly Cys Gly Ile Tyr Lys Asp Asn Asn Lys Ser Ser Ile
80 85 90

His Cys Met Asp Leu Ser Gln Arg Tyr Cys Leu Met Ala Val Phe
95 100 105

Asn Val Ile Tyr Leu Glu Asn Glu Asp Ser Glu
110 115

<210> 379

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 379

ctgcctccac tgctctgtgc tggg 24

<210> 380

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 380

cagagcagtg gatgttccccc tggg 24

<210> 381

<211> 45

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-45

<223> Synthetic construct.

<400> 381
ctgaacaaga tggtaagca agtgactggg aaaatgccca tcctc 45

<210> 382

<211> 764

<212> DNA

<213> Homo sapiens

<400> 382
ctcgttctt ccttctggat gggggccca ggggcccagg agagtataaa 50
ggcgatgtgg agggtgcccg gcacaaccag acgcccagtc acaggcgaga 100
gcccctggat gcaccggcca gaggccatgc tgctgctgct cacgcttgcc 150
ctcctgggg gcccccacctg ggcagggaaag atgtatggcc ctggaggagg 200
caagtatttc agcaccactg aagactacga ccatgaaatc acagggctgc 250
gggtgtctgt aggtcttctc ctggtgaaaa gtgtccaggt gaaacttgg 300
gactcctggg acgtgaaact gggagcccta ggtggaaata cccaggaagt 350
caccctgcag ccaggcgaat acatcacaaa agtcttgc gccttccaag 400
cttcctccg gggatggtc atgtacacca gcaaggaccg ctatttctat 450
tttgggaagc ttgatggcca gatctcctct gcctacccca gccaagaggg 500
gcaggtgctg gtggcatct atggccagta tcaactcctt ggcataaga 550
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ccagttaatc tcacatactc agcaaactca cccgtgggtc gctaggggtgg 650
ggtatgggc catccgagct gaggccatct gtgtgggtgg ggctgatgg 700
actggagtaa ctgagtcggg acgctgaatc tgaatccacc aataaataaa 750
gcttctgcag aaaa 764

<210> 383

<211> 178

<212> PRT

<213> Homo sapiens

<400> 383

Met	His	Arg	Pro	Glu	Ala	Met	Leu	Leu	Leu	Leu	Thr	Leu	Ala	Leu
1						5				10				15

Leu	Gly	Gly	Pro	Thr	Trp	Ala	Gly	Lys	Met	Tyr	Gly	Pro	Gly	Gly
						20			25				30	

Gly	Lys	Tyr	Phe	Ser	Thr	Thr	Glu	Asp	Tyr	Asp	His	Glu	Ile	Thr
								35	40				45	

Gly Leu Arg Val Ser Val Gly Leu Leu Leu Val Lys Ser Val Gln
50 55 60

Val Lys Leu Gly Asp Ser Trp Asp Val Lys Leu Gly Ala Leu Gly
65 70 75

Gly Asn Thr Gln Glu Val Thr Leu Gln Pro Gly Glu Tyr Ile Thr
80 85 90

Lys Val Phe Val Ala Phe Gln Ala Phe Leu Arg Gly Met Val Met
95 100 105

Tyr Thr Ser Lys Asp Arg Tyr Phe Tyr Phe Gly Lys Leu Asp Gly
110 115 120

Gln Ile Ser Ser Ala Tyr Pro Ser Gln Glu Gly Gln Val Leu Val
125 130 135

Gly Ile Tyr Gly Gln Tyr Gln Leu Leu Gly Ile Lys Ser Ile Gly
140 145 150

Phe Glu Trp Asn Tyr Pro Leu Glu Glu Pro Thr Thr Glu Pro Pro
155 160 165

Val Asn Leu Thr Tyr Ser Ala Asn Ser Pro Val Gly Arg
170 175

<210> 384
<211> 2379
<212> DNA
<213> Homo sapiens

<400> 384
gctgagcgtg tgcgcgtac gggctctcc tgccttctgg gctccaaacgc 50
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atacagatgt ggcagctcag gtagccccaa attgcctgga agaatacatc 150
atgttttcg ataagaagaa attgttaggat ccagttttt ttttaaccgc 200
ccccctccca ccccccaaaa aaactgtaaa gatgcaaa^{aa} cgtaatatcc 250
atgaagatcc tattacctag gaagatttg atgtttgct gcgaatgcgg 300
tgttgggatt tatttgtct tggagtgttc tgcgtggctg gcaaagaata 350
atgttccaaa atcggtccat ctcccaaggg gtccaaattt tcttcctggg 400
tgtcagcgtcag ccctgactca ctacagtgca gctgacaggg gctgtcatgc 450
aactggcccc taagccaaag caaaagaccc aaggacgacc tttgaacaat 500
acaaaggatg gtttcaatg taatttagct actgagcggc tcagctgtag 550
cactggttat agccccact gtcttactga caatgcttc ttctgccgaa 600
cgaggatgcc ctaaggcgtg taggtgtcaa ggcaaaatgg tatattgtga 650

atctcagaaa ttacaggaga taccctcaag tataatctgct ggttgcttag 700
gtttgtccct tcgctataac agccttcaaa aacttaagta taatcaattt 750
aaagggctca accagctcac ctggctatac cttgaccata accatatcag 800
caatattgac gaaaatgctt ttaatgaaat acgcagactc aaagagctga 850
ttcttagttc caatagaatc tcctatttc ttaacaatac cttcagacct 900
gtgacaaatt tacggaactt ggatctgtcc tataatcagc tgcattctct 950
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aacctggaac ttttggacct gggatataac cgatccgaa gtttagccag 1100
gaatgtctt gctggcatga tcagactcaa agaacttcac ctggagcaca 1150
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cagaaccttt acttgcagtg gaataaaatc agtgcatacg gacagaccat 1250
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cgccctcaacc tggattccaa caagctcaca tttattggtc aagagatttt 1400
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aatgcagcag aaatatttgc tcccttgtaa actggctgaa aagttttaaa 1500
ggctctaaggg agaatacaat tatctgtgcc agtcccaaag agctgcaagg 1550
agtaaatgtg atcgatgcag tgaagaacta cagcatctgt ggcaaaagta 1600
ctacagagag gtttgatctg gccaggcgc tcccaaagcc gacgtttaag 1650
cccaagctcc ccaggccgaa gcatgagagc aaacccctt tgccccgac 1700
ggtgggagcc acagagcccg gcccagagac cgatgctgac gccgagcaca 1750
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ctcgatccatcc tgctggttat ctacgtgtca tggaagcggt accctgcgag 1850
catgaagcag ctgcagcagc gctccctcat gcgaaggcac aggaaaaaga 1900
aaagacagtc cctaaagcaa atgactccca gcacccagga atttatgtta 1950
gattataaac ccaccaacac ggagaccagc gagatgctgc tgaatggac 2000
gggaccctgc acctataaca aatcgccgc cagggagtgt gaggtatgaa 2050
ccattgtgat aaaaagagct cttaaaagct gggaaataag tggtgctta 2100

ttgaactctg gtgactatca agggAACGCG atGCCCTCCC 2150
tctCCCTCTC acTTGGTGG caAGATCCTT CCTTGTCCGT TTTAGTGCAT 2200
tcataatact ggtcattttc ctctcataca taatcaaccc attgaaattt 2250
aaataccaca atcaatgtga agcttgaact ccggTTAAT ataataccta 2300
ttgtataaga ccctttactg attccattaa tgtcgcattt gttttaagat 2350
aaaacttctt tcataggtaa aaaaaaaaa 2379

<210> 385

<211> 513

<212> PRT

<213> Homo sapiens

<400> 385

Met	Gly	Phe	Asn	Val	Ile	Arg	Leu	Leu	Ser	Gly	Ser	Ala	Val	Ala
1				5					10				15	
Leu	Val	Ile	Ala	Pro	Thr	Val	Leu	Leu	Thr	Met	Leu	Ser	Ser	Ala
	20						25						30	
Glu	Arg	Gly	Cys	Pro	Lys	Gly	Cys	Arg	Cys	Glu	Gly	Lys	Met	Val
	35						40						45	
Tyr	Cys	Glu	Ser	Gln	Lys	Leu	Gln	Glu	Ile	Pro	Ser	Ser	Ile	Ser
	50							55					60	
Ala	Gly	Cys	Leu	Gly	Leu	Ser	Leu	Arg	Tyr	Asn	Ser	Leu	Gln	Lys
	65							70					75	
Leu	Lys	Tyr	Asn	Gln	Phe	Lys	Gly	Leu	Asn	Gln	Leu	Thr	Trp	Leu
	80							85					90	
Tyr	Leu	Asp	His	Asn	His	Ile	Ser	Asn	Ile	Asp	Glu	Asn	Ala	Phe
	95							100					105	
Asn	Gly	Ile	Arg	Arg	Leu	Lys	Glu	Leu	Ile	Leu	Ser	Ser	Asn	Arg
	110							115					120	
Ile	Ser	Tyr	Phe	Leu	Asn	Asn	Thr	Phe	Arg	Pro	Val	Thr	Asn	Leu
	125							130					135	
Arg	Asn	Leu	Asp	Leu	Ser	Tyr	Asn	Gln	Leu	His	Ser	Leu	Gly	Ser
	140							145					150	
Glu	Gln	Phe	Arg	Gly	Leu	Arg	Lys	Leu	Leu	Ser	Leu	His	Leu	Arg
	155							160					165	
Ser	Asn	Ser	Leu	Arg	Thr	Ile	Pro	Val	Arg	Ile	Phe	Gln	Asp	Cys
	170							175					180	
Arg	Asn	Leu	Glu	Leu	Leu	Asp	Leu	Gly	Tyr	Asn	Arg	Ile	Arg	Ser
	185							190					195	
Leu	Ala	Arg	Asn	Val	Phe	Ala	Gly	Met	Ile	Arg	Leu	Lys	Glu	Leu

200	205	210
His Leu Glu His Asn Gln Phe Ser Lys	Leu Asn Leu Ala Leu Phe	
215	220	225
Pro Arg Leu Val Ser Leu Gln Asn Leu Tyr	Leu Gln Trp Asn Lys	
230	235	240
Ile Ser Val Ile Gly Gln Thr Met Ser	Trp Thr Trp Ser Ser Leu	
245	250	255
Gln Arg Leu Asp Leu Ser Gly Asn Glu	Ile Glu Ala Phe Ser Gly	
260	265	270
Pro Ser Val Phe Gln Cys Val Pro Asn	Leu Gln Arg Leu Asn Leu	
275	280	285
Asp Ser Asn Lys Leu Thr Phe Ile Gly	Gln Glu Ile Leu Asp Ser	
290	295	300
Trp Ile Ser Leu Asn Asp Ile Ser Leu	Ala Gly Asn Ile Trp Glu	
305	310	315
Cys Ser Arg Asn Ile Cys Ser Leu Val	Asn Trp Leu Lys Ser Phe	
320	325	330
Lys Gly Leu Arg Glu Asn Thr Ile Ile	Cys Ala Ser Pro Lys Glu	
335	340	345
Leu Gln Gly Val Asn Val Ile Asp Ala	Val Lys Asn Tyr Ser Ile	
350	355	360
Cys Gly Lys Ser Thr Thr Glu Arg Phe	Asp Leu Ala Arg Ala Leu	
365	370	375
Pro Lys Pro Thr Phe Lys Pro Lys Leu	Pro Arg Pro Lys His Glu	
380	385	390
Ser Lys Pro Pro Leu Pro Pro Thr Val	Gly Ala Thr Glu Pro Gly	
395	400	405
Pro Glu Thr Asp Ala Asp Ala Glu His	Ile Ser Phe His Lys Ile	
410	415	420
Ile Ala Gly Ser Val Ala Leu Phe Leu	Ser Val Leu Val Ile Leu	
425	430	435
Leu Val Ile Tyr Val Ser Trp Lys Arg	Tyr Pro Ala Ser Met Lys	
440	445	450
Gln Leu Gln Gln Arg Ser Leu Met Arg	Arg His Arg Lys Lys	
455	460	465
Arg Gln Ser Leu Lys Gln Met Thr Pro	Ser Thr Gln Glu Phe Tyr	
470	475	480
Val Asp Tyr Lys Pro Thr Asn Thr Glu	Thr Ser Glu Met Leu Leu	
485	490	495

Asn Gly Thr Gly Pro Cys Thr Tyr Asn Lys Ser Gly Ser Arg Glu
500 505 510

Cys Glu Val

<210> 386

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 386

ctgggatctg aacagttcg gggc 24

<210> 387

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 387

ggtccccagg acatggtctg tccc 24

<210> 388

<211> 48

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-48

<223> Synthetic construct.

<400> 388

gctgagttta catttacggc ctaactccct gagaaccatc cctgtgcg 48

<210> 389

<211> 1449

<212> DNA

<213> Homo sapiens

<400> 389

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gcgatctcaa cgatagggat cttgtgttg ccgctattcc agttggtgct 150

ctcggaccta ccatgcgaag aagatgaaat gtgtgtaaat tataatgacc 200

aacaccctaa tggctggat atctggatcc tcctgctgct ggaaaaatgg 250
gcagctcttc tctgtggagc tgtggtcctc tgcctccagt gctggctgag 300
gagaccccgaa attgattctc acaggcgac catggcagtt tttgctgttg 350
gagacttgaa ctctatattt gggacagaag cagctgtgag tccaaactgtt 400
ggaattcacc ttcaaactca aaccctgac ctatatcctg ttccctgctcc 450
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caacctgatt ttaggtgtgg attatcaatt taaagtatta acgacatctg 550
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tccagagatc tattcatata gtctgaggaa ggacaattcg acaaaagaat 650
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gtagttcca tcacatttag gactccactg cagtagatacag cacaccattt 850
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ctccatagtc catagtgttt ctctggagcc tcagggcttg gcatttattg 1250
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gcagaagtag caatgagaca tcttcaagtg gcattttggc agtggccatc 1350
agcaggggaa cagacaaaaa catccatcac agatgacata tgatcttcag 1400
ctgacaaatt tggtaacaa aacaataaac atcaatagat atctaaaaa 1449

<210> 390

<211> 146

<212> PRT

<213> Homo sapiens

<400> 390

Met	Ser	Arg	Ser	Arg	Leu	Phe	Ser	Val	Thr	Ser	Ala	Ile	Ser	Thr
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Ile	Gly	Ile	Leu	Cys	Leu	Pro	Leu	Phe	Gln	Leu	Val	Leu	Ser	Asp
20														30
Leu	Pro	Cys	Glu	Glu	Asp	Glu	Met	Cys	Val	Asn	Tyr	Asn	Asp	Gln
35														45
His	Pro	Asn	Gly	Trp	Tyr	Ile	Trp	Ile	Leu	Leu	Leu	Leu	Val	Leu
50														60
Val	Ala	Ala	Leu	Leu	Cys	Gly	Ala	Val	Val	Leu	Cys	Leu	Gln	Cys
65														75
Trp	Leu	Arg	Arg	Pro	Arg	Ile	Asp	Ser	His	Arg	Arg	Thr	Met	Ala
80														90
Val	Phe	Ala	Val	Gly	Asp	Leu	Asp	Ser	Ile	Tyr	Gly	Thr	Glu	Ala
95														105
Ala	Val	Ser	Pro	Thr	Val	Gly	Ile	His	Leu	Gln	Thr	Gln	Thr	Pro
110														120
Asp	Leu	Tyr	Pro	Val	Pro	Ala	Pro	Cys	Phe	Gly	Pro	Leu	Gly	Ser
125														135
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<210> 391

<211> 26

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-26

<223> Synthetic construct.

<400> 391

ttttcagtg tcacctcagc gatctc 26

<210> 392

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 392

ccaaaacatg gagcaggaac agg 23

<210> 393

<211> 47

<212> DNA

<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-47
<223> Synthetic construct.

<400> 393
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<210> 394
<211> 2340
<212> DNA
<213> Homo sapiens

<400> 394
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gacgcagctg acgccccctt attagctctc gctgcgtcgc cccggctcag 150
aagctccgtg gcggcggcga ccgtgacgag aagcccacgg ccagctcagt 200
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ctcttcaaaa ctcatctcct gggtgactga gttaatagag tggataacaac 300
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ttttcaagtc ttgatttgg gcttacctca agttaccatt tttcagtcaa 400
gtctgtttgt ttgcttcttc agaaatgttt tttacaatct caagaaaaaa 450
tatgtcccgaa aatttgagtt tactgttgct tgtatggaa ctcatttggg 500
gattgatgtt actgcactat acttttcaac aaccaagaca tcaaaggcagt 550
gtcaagttac gtgagcaaat actagactta agcaaaagat atgttaaagc 600
tcttagcagag gaaaataaga acacagtgg atgtcgagaac ggtgcttcta 650
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attttgcac gattgggtgaa gctggagaac aaagttgact atattgtgt 750
gaatggctca gcagccaaca ccaccaatgg tactagtggg aatttggcgc 800
cagtaaccac aaataaaaga acgaatgtct cggcagttt cagatagcag 850
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<210> 395

<211> 140

<212> PRT

<213> Homo sapiens

<400> 395

Met	Phe	Phe	Thr	Ile	Ser	Arg	Lys	Asn	Met	Ser	Gln	Lys	Leu	Ser
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Leu Leu Leu Leu Val Phe Gly Leu Ile Trp Gly Leu Met Leu Leu
20 25 30

His Tyr Thr Phe Gln Gln Pro Arg His Gln Ser Ser Val Lys Leu
35 40 45

Arg Glu Gln Ile Leu Asp Leu Ser Lys Arg Tyr Val Lys Ala Leu
50 55 60

Ala Glu Glu Asn Lys Asn Thr Val Asp Val Glu Asn Gly Ala Ser
65 70 75

Met Ala Gly Tyr Ala Asp Leu Lys Arg Thr Ile Ala Val Leu Leu
80 85 90

Asp Asp Ile Leu Gln Arg Leu Val Lys Leu Glu Asn Lys Val Asp
95 100 105

Tyr Ile Val Val Asn Gly Ser Ala Ala Asn Thr Thr Asn Gly Thr
110 115 120

Ser Gly Asn Leu Val Pro Val Thr Thr Asn Lys Arg Thr Asn Val
125 130 135

Ser Gly Ser Ile Arg
140

<210> 396
<211> 2639
<212> DNA
<213> Homo sapiens

<400> 396
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acttcggcc ttttcgacag cttcagcctg actcgggtgg atttagcgg 200
cctggggcccc cacatcatgc cggtgcccac ccctctggac acagccact 250
tggacctgtc ctccaaccgg ctggagatgg tgaatgagtc ggtgttggcg 300
gggcccggct acacgacgtt ggctggctg gatctcagcc acaacctgct 350
caccagcatc tcacccactg cttctcccg cttcgctac ctggagtcgc 400
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<210> 397

<211> 353

<212> PRT

<213> Homo sapiens

<400> 397

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Thr	Thr	Arg	Pro	Cys	Phe	Pro	Gly	Cys	Gln	Cys	Glu	Val	Glu	Thr
				20				25				30		
Phe	Gly	Leu	Phe	Asp	Ser	Phe	Ser	Leu	Thr	Arg	Val	Asp	Cys	Ser
				35				40				45		
Gly	Leu	Gly	Pro	His	Ile	Met	Pro	Val	Pro	Ile	Pro	Leu	Asp	Thr
				50				55				60		
Ala	His	Leu	Asp	Leu	Ser	Ser	Asn	Arg	Leu	Glu	Met	Val	Asn	Glu
				65				70				75		
Ser	Val	Leu	Ala	Gly	Pro	Gly	Tyr	Thr	Thr	Leu	Ala	Gly	Leu	Asp
				80				85				90		
Leu	Ser	His	Asn	Leu	Leu	Thr	Ser	Ile	Ser	Pro	Thr	Ala	Phe	Ser
				95				100				105		
Arg	Leu	Arg	Tyr	Leu	Glu	Ser	Leu	Asp	Leu	Ser	His	Asn	Gly	Leu
				110				115				120		
Thr	Ala	Leu	Pro	Ala	Glu	Ser	Phe	Thr	Ser	Ser	Pro	Leu	Ser	Asp
				125				130				135		
Val	Asn	Leu	Ser	His	Asn	Gln	Leu	Arg	Glu	Val	Ser	Val	Ser	Ala
				140				145				150		

Phe	Thr	Thr	His	Ser	Gln	Gly	Arg	Ala	Leu	His	Val	Asp	Leu	Ser
														165
155														
His	Asn	Leu	Ile	His	Arg	Leu	Val	Pro	His	Pro	Thr	Arg	Ala	Gly
														180
170														
Leu	Pro	Ala	Pro	Thr	Ile	Gln	Ser	Leu	Asn	Leu	Ala	Trp	Asn	Arg
														195
185														
Leu	His	Ala	Val	Pro	Asn	Leu	Arg	Asp	Leu	Pro	Leu	Arg	Tyr	Leu
														210
200														
Ser	Leu	Asp	Gly	Asn	Pro	Leu	Ala	Val	Ile	Gly	Pro	Gly	Ala	Phe
														225
215														
Ala	Gly	Leu	Gly	Gly	Leu	Thr	His	Leu	Ser	Leu	Ala	Ser	Leu	Gln
														240
230														
Arg	Leu	Pro	Glu	Leu	Ala	Pro	Ser	Gly	Phe	Arg	Glu	Leu	Pro	Gly
														255
245														
Leu	Gln	Val	Leu	Asp	Leu	Ser	Gly	Asn	Pro	Lys	Leu	Asn	Trp	Ala
														270
260														
Gly	Ala	Glu	Val	Phe	Ser	Gly	Leu	Ser	Ser	Leu	Gln	Glu	Leu	Asp
														285
275														
Leu	Ser	Gly	Thr	Asn	Leu	Val	Pro	Leu	Pro	Glu	Ala	Leu	Leu	Leu
														300
290														
His	Leu	Pro	Ala	Leu	Gln	Ser	Val	Ser	Val	Gly	Gln	Asp	Val	Arg
														315
305														
Cys	Arg	Arg	Leu	Val	Arg	Glu	Gly	Thr	Tyr	Pro	Arg	Arg	Pro	Gly
														330
320														
Ser	Ser	Pro	Lys	Val	Pro	Leu	His	Cys	Val	Asp	Thr	Arg	Glu	Ser
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335														
Ala	Ala	Arg	Gly	Pro	Thr	Ile	Leu							
350														

<210> 398

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 398

ccctgccagc cgagagcttc acc 23

<210> 399

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 399
ggttgggcc cgaaaggtcc agc 23

<210> 400

<211> 44

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-44

<223> Synthetic construct.

<400> 400
caaccccaag cttaactggg caggagctga ggtgtttca ggcc 44

<210> 401

<211> 1571

<212> DNA

<213> Homo sapiens

<400> 401
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gaggctataat gcgtcaattc cccaaaacaa gtttgacat ttcccctgaa 150
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tgtggaaataa gtttgatgt ggaattgcac atctaccttca caattactga 1450
ccatccccag tagactcccc agtcccataa ttgtgtatct tccagccagg 1500
aatcctacac ggccagcatg tatttctaca aataaagttt tctttgcata 1550
ccaaaaaaaaaaaaaaa a 1571

<210> 402

<211> 261

<212> PRT

<213> Homo sapiens

<400> 402

Met	Arg	Gln	Phe	Pro	Lys	Thr	Ser	Phe	Asp	Ile	Ser	Pro	Glu	Met
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Ser	Phe	Ser	Ile	Tyr	Ser	Leu	Gln	Val	Pro	Ala	Val	Pro	Gly	Leu
				20					25				30	

Thr	Cys	Trp	Ala	Leu	Thr	Ala	Glu	Pro	Gly	Trp	Gly	Gln	Asn	Lys
				35				40				45		

Gly	Ala	Thr	Thr	Cys	Ala	Thr	Asn	Ser	His	Ser	Asp	Ser	Glu	Leu
				50				55				60		

Arg	Pro	Glu	Ile	Phe	Ser	Ser	Arg	Glu	Ala	Trp	Gln	Phe	Phe	Leu
			65					70				75		

Leu	Leu	Trp	Ser	Pro	Asp	Phe	Arg	Pro	Lys	Met	Lys	Ala	Ser	Ser
			80					85				90		

Leu	Ala	Phe	Ser	Leu	Leu	Ser	Ala	Ala	Phe	Tyr	Leu	Leu	Trp	Thr
95									100				105	
Pro	Ser	Thr	Gly	Leu	Lys	Thr	Leu	Asn	Leu	Gly	Ser	Cys	Val	Ile
				110					115				120	
Ala	Thr	Asn	Leu	Gln	Glu	Ile	Arg	Asn	Gly	Phe	Ser	Glu	Ile	Arg
				125					130				135	
Gly	Ser	Val	Gln	Ala	Lys	Asp	Gly	Asn	Ile	Asp	Ile	Arg	Ile	Leu
				140					145				150	
Arg	Arg	Thr	Glu	Ser	Leu	Gln	Asp	Thr	Lys	Pro	Ala	Asn	Arg	Cys
				155					160				165	
Cys	Leu	Leu	Arg	His	Leu	Leu	Arg	Leu	Tyr	Leu	Asp	Arg	Val	Phe
				170					175				180	
Lys	Asn	Tyr	Gln	Thr	Pro	Asp	His	Tyr	Thr	Leu	Arg	Lys	Ile	Ser
				185					190				195	
Ser	Leu	Ala	Asn	Ser	Phe	Leu	Thr	Ile	Lys	Lys	Asp	Leu	Arg	Leu
				200					205				210	
Ser	His	Ala	His	Met	Thr	Cys	His	Cys	Gly	Glu	Glu	Ala	Met	Lys
				215					220				225	
Lys	Tyr	Ser	Gln	Ile	Leu	Ser	His	Phe	Glu	Lys	Leu	Glu	Pro	Gln
				230					235				240	
Ala	Ala	Val	Val	Lys	Ala	Leu	Gly	Glu	Leu	Asp	Ile	Leu	Leu	Gln
				245					250				255	
Trp	Met	Glu	Glu	Thr	Glu									
				260										

<210> 403

<211> 28

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-28

<223> Synthetic construct.

<400> 403

ctcctgtggc ctccagattt caggccta 28

<210> 404

<211> 26

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-26

<223> Synthetic construct.

<400> 404
agtccctcctt aagattctga tgtcaa 26

<210> 405
<211> 998
<212> DNA
<213> Homo sapiens

<400> 405
cggttatcgt cttgcgtac tgctgaatgt ccgtcccgga ggaggaggag 50
aggctttgc cgctgaccca gagatggccc cgagcgagca aattcctact 100
gtccggctgc gggcttaccg tggccgagct agcaaccttt cccctggatc 150
tcacaaaaac tcgactccaa atgcaaggag aagcagctct tgctcggttg 200
ggagacggtg caagagaatc tgcccccattt agggaaatgg tgcgcacagc 250
cctagggatc attgaagagg aaggctttctt aaagctttgg caaggagtga 300
cacccgccat ttacagacac gtatgttattt ctggaggtcg aatggtcaca 350
tatgaacatc tccgagaggt tgcgtttggc aaaagtgaag atgagcatta 400
tcccccttgg aaatcagtca ttggagggat gatggctgggt gttattggcc 450
agtttttagc caatccaact gacctagtga aggttcagat gcaaatggaa 500
ggaaaaagga aactggaagg aaaaccattt cgatttcgtg gtgtacatca 550
tgcatttgca aaaatcttag ctgaaggagg aatacgaggg ctttggcag 600
gctgggtacc caatatacaa agagcagcac tggtaatat gggagattta 650
accacttatg atacagtcaa acactacttgc gtattgaata caccacttga 700
ggacaatatac atgactcactg gtttatcaag tttatgttct ggactggtag 750
cttctattctt gggAACACCA gcccgtatgtca tcaaaAGCAG aataatgaat 800
caaccacgag ataaaacaagg aaggggactt ttgtataat catcgactga 850
ctgcttgattt caggctgttc aaggtgaagg attcatgagt ctatataaag 900
gcttttacc atcttggctg agaatgaccc cttggtaat ggtgttctgg 950
cttacttatg aaaaatcag agagatgagt ggagtcagtc cattttaa 998

<210> 406
<211> 323
<212> PRT
<213> Homo sapiens

<400> 406
Met Ser Val Pro Glu Glu Glu Glu Arg Leu Leu Pro Leu Thr Gln
1 5 10 15

Arg Trp Pro Arg Ala Ser Lys Phe Leu Leu Ser Gly Cys Ala Ala
 20 25 30

Thr Val Ala Glu Leu Ala Thr Phe Pro Leu Asp Leu Thr Lys Thr
 35 40 45

Arg Leu Gln Met Gln Gly Glu Ala Ala Leu Ala Arg Leu Gly Asp
 50 55 60

Gly Ala Arg Glu Ser Ala Pro Tyr Arg Gly Met Val Arg Thr Ala
 65 70 75

Leu Gly Ile Ile Glu Glu Gly Phe Leu Lys Leu Trp Gln Gly
 80 85 90

Val Thr Pro Ala Ile Tyr Arg His Val Val Tyr Ser Gly Gly Arg
 95 100 105

Met Val Thr Tyr Glu His Leu Arg Glu Val Val Phe Gly Lys Ser
 110 115 120

Glu Asp Glu His Tyr Pro Leu Trp Lys Ser Val Ile Gly Gly Met
 125 130 135

Met Ala Gly Val Ile Gly Gln Phe Leu Ala Asn Pro Thr Asp Leu
 140 145 150

Val Lys Val Gln Met Gln Met Glu Gly Lys Arg Lys Leu Glu Gly
 155 160 165

Lys Pro Leu Arg Phe Arg Gly Val His His Ala Phe Ala Lys Ile
 170 175 180

Leu Ala Glu Gly Gly Ile Arg Gly Leu Trp Ala Gly Trp Val Pro
 185 190 195

Asn Ile Gln Arg Ala Ala Leu Val Asn Met Gly Asp Leu Thr Thr
 200 205 210

Tyr Asp Thr Val Lys His Tyr Leu Val Leu Asn Thr Pro Leu Glu
 215 220 225

Asp Asn Ile Met Thr His Gly Leu Ser Ser Leu Cys Ser Gly Leu
 230 235 240

Val Ala Ser Ile Leu Gly Thr Pro Ala Asp Val Ile Lys Ser Arg
 245 250 255

Ile Met Asn Gln Pro Arg Asp Lys Gln Gly Arg Gly Leu Leu Tyr
 260 265 270

Lys Ser Ser Thr Asp Cys Leu Ile Gln Ala Val Gln Gly Glu Gly
 275 280 285

Phe Met Ser Leu Tyr Lys Gly Phe Leu Pro Ser Trp Leu Arg Met
 290 295 300

Thr Pro Trp Ser Met Val Phe Trp Leu Thr Tyr Glu Lys Ile Arg

305

310

315

Glu Met Ser Gly Val Ser Pro Phe
320

<210> 407

<211> 31

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-31

<223> Synthetic construct.

<400> 407

cgcggatccc gttatcgctc tgcgctactg c 31

<210> 408

<211> 34

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-34

<223> Synthetic construct.

<400> 408

gcggaattct taaaatggac tgactccact catc 34

<210> 409

<211> 1487

<212> DNA

<213> Homo sapiens

<400> 409

cggacgcgtg ggcgcgggac gccggcaggg ttgtggcgca gcagtctcct 50

tcctgcgcgc ggcgcctgaag tcggcgtggg cgttttagga agctggata 100

cagcatttaa tgaaaaattt atgcttaaga agtaaaaatg gcaggcttcc 150

tagataattt tcgttggcca gaatgtaat gtattgactg gagtgagaga 200

agaaatgctg tggcatctgt tgtcgcaggat atattgtttt ttacaggctg 250

gtggataatg attgatgcag ctgtgggtga tcctaagcca gaacagttga 300

accatgcctt tcacacatgt ggtgtatattt ccacattggc tttcttcatg 350

ataaaatgctg tatccaatgc tcaggtgaga ggtgatagct atgaaagcgg 400

ctgttttagga agaacaggtg ctcgagtttgcgttccatt ggtttcatgt 450

tgtatgtttgg gtcacttatt gcttccatgt ggattcttt tggtgcataat 500

gttacccaaa atactgatgt ttatccggga ctagctgtgt ttttcaaaa 550

tgcaactata ttttttagca ctctgatcta caaatttgg a agaaccgaag 600
agctatggac ctgagatcac ttcttaagtc acatttcct tttgttatat 650
tctgttgta gataggtttt ttatctctca gtacacattg ccaaatggag 700
tagattgtac attaaatgtt ttgtttctt acattttat gttctgagtt 750
ttgaaatagt tttatgaaat ttctttattt ttcattgcat agactgttaa 800
tatgtatata atacaagact atatgaattt gataatgagt atcagtttt 850
tattcctgag attagaact tgatctactc cctgagccag ggttacatca 900
tcttgcatt ttagaagtaa ccactcttgc ctctctggct gggcacggg 950
gctcatgcct gtaatcccag cactttggga ggccgaggcg ggccgattgc 1000
ttgaggtcaa gtgttgaga ccagcctggc caacatggcg aaaccccatc 1050
tactaaaaat acaaaaatta gccaggcatg gtggtgggtg cctgtaatcc 1100
cagctacctg ggaggctgag gcaggagaat cgcttgaacc cggggggcag 1150
aggttgcagt gagctgagtt tgcgccactg cactctagcc tgggggagaa 1200
agtgaaactc cctctcaaaa aaaagaccac tctcagttatc tctgatttct 1250
gaagatgtac aaaaaaatat agttcatat atctggaatg agcaactgagc 1300
cataaaaggt tttcagcaag ttgttaactt ttttggcta aaaatgaggt 1350
tttttggta aagaaaaat atttgttctt atgtattgaa gaagtgtact 1400
tttatataat gatttttaa atgccccaaag gactagttt 1450
ttaaaaagaa ttcctcta atgactttat gtgagaa 1487

<210> 410

<211> 158

<212> PRT

<213> Homo sapiens

<400> 410

Met	Ala	Gly	Phe	Leu	Asp	Asn	Phe	Arg	Trp	Pro	Glu	Cys	Glu	Cys
1										10				15
Ile	Asp	Trp	Ser	Glu	Arg	Arg	Asn	Ala	Val	Ala	Ser	Val	Val	Ala
									20		25		30	
Gly	Ile	Leu	Phe	Phe	Thr	Gly	Trp	Trp	Ile	Met	Ile	Asp	Ala	Ala
									35		40		45	
Val	Val	Tyr	Pro	Lys	Pro	Glu	Gln	Leu	Asn	His	Ala	Phe	His	Thr
									50		55		60	
Cys	Gly	Val	Phe	Ser	Thr	Leu	Ala	Phe	Phe	Met	Ile	Asn	Ala	Val
									65		70		75	

Ser Asn Ala Gln Val Arg Gly Asp Ser Tyr Glu Ser Gly Cys Leu
80 85 90
Gly Arg Thr Gly Ala Arg Val Trp Leu Phe Ile Gly Phe Met Leu
95 100 105
Met Phe Gly Ser Leu Ile Ala Ser Met Trp Ile Leu Phe Gly Ala
110 115 120
Tyr Val Thr Gln Asn Thr Asp Val Tyr Pro Gly Leu Ala Val Phe
125 130 135
Phe Gln Asn Ala Leu Ile Phe Phe Ser Thr Leu Ile Tyr Lys Phe
140 145 150
Gly Arg Thr Glu Glu Leu Trp Thr
155

<210> 411
<211> 20
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-20
<223> Synthetic construct.

<400> 411
gttgaggaa gctggatac 20

<210> 412
<211> 20
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-20
<223> Synthetic construct.

<400> 412
ccaaactcga gcacctgttc 20

<210> 413
<211> 40
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-40
<223> Synthetic construct.

<400> 413
atggcaggct tcctagataa ttttcgttgg ccagaatgtg 40

<210> 414

<211> 1337
<212> DNA
<213> Homo sapiens

<400> 414
gttgcgtggca aacttcctca aaggaggggc agagcctgcg cagggcagga 50
gcagctggcc cactggcgcc ccgcaacact ccgtctcacc ctctgggccc 100
actgcacatca gaggaggggcc gtctgtgagg ccactacccc tccagcaact 150
gggaggtggg actgtcagaa gctggcccaag ggtgggtggc agctgggtca 200
gggacacctacg gcacactgctg gaccacctcg ccttctccat cgaagcaggg 250
aagtgggagc ctcgagccct cgggtggaaag ctgaccccaa gccacccttc 300
acctggacacag gatgagagtg tcaggtgtgc ttgcctcctt ggcctcatac 350
tttgcctatag tcacgacatg gatgtttatt cgaagctaca tgagcttcag 400
catgaaaacc atccgtctgc cacgctggct ggcagcctcg cccaccaagg 450
agatccaggt taaaaagtac aagtgtggcc tcatcaagcc ctgcccagcc 500
aactacttg cggttaaat ctgcagtggg gccgccaacg tcgtgggccc 550
tactatgtgc tttgaagacc gcatgatcat gagtcctgtg aaaaacaatg 600
tgggcagagg cctaaacatc gccctggtga atgaaaccac gggagctgtg 650
ctgggacaga aggcatattga catgtactct ggagatgtta tgcacctagt 700
gaaattcctt aaagaaaattc cgggggggtgc actggtgctg gtggcctcct 750
acgacgatcc agggaccaaa atgaacgatg aaagcaggaa actcttctct 800
gacttgggga gttcctacgc aaaacaactg ggcttccggg acagctgggt 850
cttcatagga gccaaagacc tcagggtaa aagcccttt gagcagttct 900
taaagaacag cccagacaca aacaaatacg agggatggcc agagctgctg 950
gagatggagg gctgcacgcc cccgaagcca ttttagggtg gctgtggctc 1000
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cccgccaggg gctgaggagg aggagcaggg ggtgctgcgt ggaagggtgct 1100
gcaggtcctt gcacgctgtg tcgcgcctct cctcctcgga aacagaaccc 1150
tcccacagca catcctaccc ggaagaccag cctcagaggg tccttctgga 1200
accagctgtc tgtggagaga atgggggtgct ttgcgtcaggg actgctgacg 1250
gctggtcctg aggaaggaca aactgcccag acttgagccc aattaaattt 1300
tatttttgct gggtttgaaa aaaaaaaaaa aaaaaaaaa 1337

<210> 415
<211> 224
<212> PRT
<213> Homo sapiens

<400> 415
Met Arg Val Ser Gly Val Leu Arg Leu Leu Ala Leu Ile Phe Ala
1 5 10 15
Ile Val Thr Thr Trp Met Phe Ile Arg Ser Tyr Met Ser Phe Ser
20 25 30
Met Lys Thr Ile Arg Leu Pro Arg Trp Leu Ala Ala Ser Pro Thr
35 40 45
Lys Glu Ile Gln Val Lys Lys Tyr Lys Cys Gly Leu Ile Lys Pro
50 55 60
Cys Pro Ala Asn Tyr Phe Ala Phe Lys Ile Cys Ser Gly Ala Ala
65 70 75
Asn Val Val Gly Pro Thr Met Cys Phe Glu Asp Arg Met Ile Met
80 85 90
Ser Pro Val Lys Asn Asn Val Gly Arg Gly Leu Asn Ile Ala Leu
95 100 105
Val Asn Gly Thr Thr Gly Ala Val Leu Gly Gln Lys Ala Phe Asp
110 115 120
Met Tyr Ser Gly Asp Val Met His Leu Val Lys Phe Leu Lys Glu
125 130 135
Ile Pro Gly Gly Ala Leu Val Leu Val Ala Ser Tyr Asp Asp Pro
140 145 150
Gly Thr Lys Met Asn Asp Glu Ser Arg Lys Leu Phe Ser Asp Leu
155 160 165
Gly Ser Ser Tyr Ala Lys Gln Leu Gly Phe Arg Asp Ser Trp Val
170 175 180
Phe Ile Gly Ala Lys Asp Leu Arg Gly Lys Ser Pro Phe Glu Gln
185 190 195
Phe Leu Lys Asn Ser Pro Asp Thr Asn Lys Tyr Glu Gly Trp Pro
200 205 210
Glu Leu Leu Glu Met Glu Gly Cys Met Pro Pro Lys Pro Phe
215 220

<210> 416
<211> 21
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence

<222> 1-21
<223> Synthetic construct.

<400> 416
gccccatgtca cgacatggat g 21

<210> 417
<211> 18
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 417
ggatggccag agctgctg 18

<210> 418
<211> 26
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-26
<223> Synthetic construct.

<400> 418
aaagtacaag tgtggcctca tcaaggc 26

<210> 419
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 419
tctgactcct aagtcaaggca ggag 24

<210> 420
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 420
attctctcca cagacagctg gtcc 24

<210> 421
<211> 46
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-46
<223> Synthetic construct.

<400> 421
gtacaagtgt ggcctcatca agccctgccc agccaactac tttgcg 46

<210> 422
<211> 1701
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 1528
<223> unknown base

<400> 422
gagactgcag agggagataa agagagaggg caaagaggca gcaagagatt 50
tgtcctgggg atccagaaac ccatgatacc ctactgaaca ccgaatcccc 100
tggaaagccca cagagacaga gacagcaaga gaagcagaga taaatacact 150
cacgccagga gctcgctcgc tctctctctc tctctctcac tcctccctcc 200
ctctctctct gcctgtccta gtcctctagt cctcaaattc ccagtcctcc 250
gcaccccttc ctgggacact atgttgttct ccgcctcct gctggaggtg 300
atttggatcc tggctgcaga tgggggtcaa cactggacgt atgagggccc 350
acatggtcag gaccattggc cagccttta ccctgagtgt ggaaacaatg 400
cccagtcgcc catcgatatt cagacagaca gtgtgacatt tgaccctgat 450
ttgcctgctc tgcagccca cggatatgac cagcctggca ccgagcctt 500
ggacctgcac aacaatggcc acacagtgcac actctctctg ccctctaccc 550
tgtatctggg tggacttccc cgaaaatatg tagctgccc gctccacctg 600
cactgggtc agaaaggatc cccagggggg tcagaacacc agatcaacag 650
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atgacagctt gagtgaggct gctgagaggc ctcagggcct ggctgtcctg 750
ggcatcctaa ttgaggtggg tgagactaag aatatacgat atgaacacat 800
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ctcccttcaa cctaagagag ctgctcccc aacagctggg gcagtacttc 900
cgctacaatg gctcgctcac aactccccct tgctaccaga gtgtgctctg 950
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catggatgtg gatgacttcc cttcatgcct atcaggaagc ctctaaaatg 1350
gggtgttagga tctggccaga aacactgttag gagtagtaag cagatgtcct 1400
ccttccccctg gacatctctt agagaggaat ggaccaggc tgtcattcca 1450
ggaagaactg cagagccttc agcctctcca aacatgtagg aggaaatgag 1500
gaaatcgctg tggatggat gcagagana aactctgttt agttgcaggg 1550
gaagtttggg atataccca aagtcctcta cccctcaact tttatggccc 1600
tttccctaga tataactgcgg gatctctcct taggataaag agttgctgtt 1650
gaagttgtat attttgcgt aatataattt gaaattaaag tttctgactt 1700
t 1701

<210> 423
<211> 337
<212> PRT
<213> Homo sapiens

<400> 423
Met Leu Phe Ser Ala Leu Leu Leu Glu Val Ile Trp Ile Leu Ala
1 5 10 15
Ala Asp Gly Gly Gln His Trp Thr Tyr Glu Gly Pro His Gly Gln
20 25 30
Asp His Trp Pro Ala Ser Tyr Pro Glu Cys Gly Asn Asn Ala Gln
35 40 45
Ser Pro Ile Asp Ile Gln Thr Asp Ser Val Thr Phe Asp Pro Asp
50 55 60
Leu Pro Ala Leu Gln Pro His Gly Tyr Asp Gln Pro Gly Thr Glu
65 70 75
Pro Leu Asp Leu His Asn Asn Gly His Thr Val Gln Leu Ser Leu

80	85	90
Pro Ser Thr Leu Tyr	Leu Gly Gly	Leu Pro Arg Lys Tyr Val Ala
95	100	105
Ala Gln Leu His Leu His	Trp Gly Gln Lys Gly Ser Pro Gly	Gly
110	115	120
Ser Glu His Gln Ile Asn Ser Glu Ala	Thr Phe Ala Glu Leu His	
125	130	135
Ile Val His Tyr Asp Ser Asp Ser Tyr	Asp Ser Leu Ser Glu Ala	
140	145	150
Ala Glu Arg Pro Gln Gly	Leu Ala Val Leu Gly Ile Leu Ile Glu	
155	160	165
Val Gly Glu Thr Lys Asn Ile Ala Tyr	Glu His Ile Leu Ser His	
170	175	180
Leu His Glu Val Arg His Lys Asp Gln Lys	Thr Ser Val Pro Pro	
185	190	195
Phe Asn Leu Arg Glu Leu Leu Pro Lys	Gln Leu Gly Gln Tyr Phe	
200	205	210
Arg Tyr Asn Gly Ser Leu Thr Thr Pro	Pro Cys Tyr Gln Ser Val	
215	220	225
Leu Trp Thr Val Phe Tyr Arg Arg Ser	Gln Ile Ser Met Glu Gln	
230	235	240
Leu Glu Lys Leu Gln Gly Thr Leu Phe	Ser Thr Glu Glu Glu Pro	
245	250	255
Ser Lys Leu Leu Val Gln Asn Tyr Arg	Ala Leu Gln Pro Leu Asn	
260	265	270
Gln Arg Met Val Phe Ala Ser Phe Ile	Gln Ala Gly Ser Ser Tyr	
275	280	285
Thr Thr Gly Glu Met Leu Ser Leu Gly	Val Gly Ile Leu Val Gly	
290	295	300
Cys Leu Cys Leu Leu Ala Val Tyr	Phe Ile Ala Arg Lys Ile	
305	310	315
Arg Lys Lys Arg Leu Glu Asn Arg Lys	Ser Val Val Phe Thr Ser	
320	325	330
Ala Gln Ala Thr Thr Glu Ala		
335		

<210> 424
 <211> 18
 <212> DNA
 <213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 424
gtaaagtgc tggccagc 18

<210> 425
<211> 18
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 425
cccgatctgc ctgctgta 18

<210> 426
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 426
ctgcactgta tggccattat tgtg 24

<210> 427
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 427
cagaaaaccca tgatacccta ctgaacacccg aatcccctgg aagcc 45

<210> 428
<211> 1073
<212> DNA
<213> Homo sapiens

<400> 428
aattttcac cagagtaaac ttgagaaacc aactggacct tgagtattgt 50
acatttgcc tcgtggaccc aaaggtagca atctgaaaca tgaggagtag 100
gattctactg tttgtcttc taggatcaac tcggtcatta ccacagctca 150

aacctgctt gggactccct cccacaaaac tggctccgga tcagggaca 200
ctaccaaacc aacagcagtc aaatcaggtc tttccttctt taagtctgat 250
accattaaca cagatgctca cactggggcc agatctgcat ctgttaaattc 300
ctgctgcagg aatgacacactt ggtacccaga cccacccatt gaccctggga 350
gggttgaatg tacaacagca actgcaccca catgtgttac caattttgt 400
cacacaactt ggagcccagg gcactatcct aagctcagag gaattgccac 450
aaatcttcac gagcctcatc atccattcct tggccggg aggcatcctg 500
cccaccagtc aggcaaaaaa taatccagat gtccaggatg gaagccttcc 550
agcaggagga gcaggtgtaa atcctgccac ccagggaaacc ccagcaggcc 600
gcctcccaac tcccagtggc acagatgacg actttcagt gaccacccct 650
gcaggcatcc aaaggagcac acatgccatc gaggaagcca ccacagaatc 700
agcaaatgga attcagtaag ctgtttcaaa tttttcaac taagctgcct 750
cgaatttggt gatacatgtg aatctttatc attgattata ttatggaata 800
gattgagaca cattggatag tcttagaaga aattaattct taatttacct 850
gaaaatattc ttgaaatttc agaaaatatg ttctatgttag agaatccaa 900
ctttaaaaaa caataattca atggataat ctgtcttga aatataacat 950
tatgctgcct ggatgatatg catattaaaa catatttggaa aaactggaaa 1000
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1050
aaaaaaaaaa aaaaaaaaaa aaa 1073

<210> 429

<211> 209

<212> PRT

<213> Homo sapiens

<400> 429

Met	Arg	Ser	Thr	Ile	Leu	Leu	Phe	Cys	Leu	Leu	Gly	Ser	Thr	Arg
1				5					10				15	
Ser	Leu	Pro	Gln	Leu	Lys	Pro	Ala	Leu	Gly	Leu	Pro	Pro	Thr	Lys
					20				25				30	
Leu	Ala	Pro	Asp	Gln	Gly	Thr	Leu	Pro	Asn	Gln	Gln	Gln	Ser	Asn
				35					40				45	
Gln	Val	Phe	Pro	Ser	Leu	Ser	Leu	Ile	Pro	Leu	Thr	Gln	Met	Leu
					50				55				60	
Thr	Leu	Gly	Pro	Asp	Leu	His	Leu	Leu	Asn	Pro	Ala	Ala	Gly	Met
					65				70				75	

Thr	Pro	Gly	Thr	Gln	Thr	His	Pro	Leu	Thr	Leu	Gly	Gly	Leu	Asn
														90
80									85					
Val	Gln	Gln	Gln	Leu	His	Pro	His	Val	Leu	Pro	Ile	Phe	Val	Thr
														105
									100					
Gln	Leu	Gly	Ala	Gln	Gly	Thr	Ile	Leu	Ser	Ser	Glu	Glu	Leu	Pro
														120
									115					
Gln	Ile	Phe	Thr	Ser	Leu	Ile	Ile	His	Ser	Leu	Phe	Pro	Gly	Gly
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									130					
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35 40 45
Glu Val Val Asp Leu Tyr Asn Gly Met Cys Ile Gln Gly Pro Ala
50 55 60
Gly Val Pro Gly Arg Asp Gly Ser Pro Gly Ala Asn Val Ile Pro
65 70 75
Gly Thr Pro Gly Ile Pro Gly Arg Asp Gly Phe Lys Gly Glu Lys
80 85 90
Gly Glu Cys Leu Arg Glu Ser Phe Glu Glu Ser Trp Thr Pro Asn
95 100 105
Tyr Lys Gln Cys Ser Trp Ser Ser Leu Asn Tyr Gly Ile Asp Leu
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Gly Lys Ile Ala Glu Cys Thr Phe Thr Lys Met Arg Ser Asn Ser
125 130 135

Ala Leu Arg Val Leu Phe Ser Gly Ser Leu Arg Leu Lys Cys Arg
140 145 150
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155 160 165
Cys Ser Gly Pro Leu Pro Ile Glu Ala Ile Ile Tyr Leu Asp Gln
170 175 180
Gly Ser Pro Glu Met Asn Ser Thr Ile Asn Ile His Arg Thr Ser
185 190 195
Ser Val Glu Gly Leu Cys Glu Gly Ile Gly Ala Gly Leu Val Asp
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